

FIGURE 1

ACTGCACCTCGGTTCTATCGATTGAATTCCCCGGGGATCCTCTAGAGATCCCTGACCTCGA
CCCACCGCGTCCGGGCGGAGCAGCACGGCGCAGGACCTGGAGCTCCGGCTGCGTCTCCCG
CAGCGCTACCGCCATGCGCTGCCGCCGGGGCGCTGGGGCTCTGCCGCTTCTGCTG
CTGCTGCCGCCGCCGGAGGCCAAGAAGCCGACGCCCTGCCACCGGTGCCGGGGCT
GGTGGACAAGTTAACCAAGGGGATGGTGGACACCGCAAAGAAGAAACTTGGCGGCGGGAAACA
CGGCTTGGGAGGAAAAGACGCTGTCCAAGTACAGTCCAGCGAGATTGCCCTGCTGGAGATC
CTGGAGGGGCTGTGCGAGAGCAGCGACTTCGAATGCAATCAGATGCTAGAGGCGCAGGAGGA
GCACCTGGAGGCCTGGCTGAGCTGAAGAGCGAATATCCTGACTTATTGAGTGGTTTT
GTGTGAAGACACTGAAAGTGTGCTGCTCCAGGAACCTACGGTCCCAGTGTCTCGCATGC
CAGGGCGGATCCCAGAGGCCCTGAGCGGAATGGCAGTGCAGCGGAGATGGAGCAGACA
GGGGCAGGGCTCTGGCTGAGGCCATGGGTACAGGGCCGCTGTGCACTGACTGCATGG
ACGGCTACTTCAGCTCGCTCCGAACGAGACCCACAGCATCTGCACAGCCTGTGACGAGTCC
TGCAAGACGTGCTCGGGCTGACCAACAGAGACTGCGCGAGTGTGAAGTGGCTGGGTGCT
GGACGAGGGCGCTGTGAGTGTGAGCTGCGGGCCAGCCCTCCCTGCAGCGCTG
CGCAGTTCTGTAAGAACGCCAACGGCTCTACACGTGCGAAGAGTGTGACTCCAGCTGTG
GGCTGACAGGGGAGGCCAGGAAACTGTAAGAGTGTATCTCTGGCTACGCGAGGGAGCA
CGGACAGTGTGCAAGTGTGAGCTACTAGCAGAAAAACCTGTGTGAGGAAAAACG
AAAAGTGTACAATACTCAGGGAGCTACGTCTGTGTGCTGAGGGCTTCGAAGAACG
GAAGATGCGTGTGCGCCGGCAGAGGCTGAAGCCACAGAAGGAGAAAGCCGACAGCT
GCCCTCCCGGAAGACCTGTAATGTGCGGACTTACCCCTAAATTATTGAGAAGATGTCC
CGTGGAAATGTGGCCCTGAGGATGCCGCTCTGCAGTGGACAGCGGGGGAGAGGCTGC
CTGCTCTAAGGGTGATTCTATTGTCCTAAACAGCTGCATTCTGGTTGTTCTTA
AACAGACTGTATATTTGATACAGTTCTTGTAAATAAAATTGACCATTGTAGGTAATCAGG
AGGAAAAAAAGGGCGCCCGCAGACTCTAGAGTCGACCTGCAAGC
TTGGCCGCATGGCCAACCTGTTATTGAGCTTAAATGGTTACAATAAGCAATAGCA
TCACAAATTTCACAAATAAACGATTTCAGTGCATTCTAGTTGTGGTTGTCCAAACTC
ATCAATGTATCTTATCATGTCGGATGGGAATTAACTGGCGCAGCACCATGGCTGAAAT
AACCTCTGAAGAGGAACCTGGTAGGTAACCTCTGAGGCGGAAAGAACCCAGCTGTGAAATG
TGTGTCAGTTAGGGTGTGGAAAGTCCCCAGGCTCCCCAGCAGGAGAAGTATGCAAGCATGC
ATCTCAATTAGTCAGCAACCCAGTTT

FIGURE 2

><subunit 1 of 1, 353 aa, 0 stop

><MW: 38192, PI: 4.53, NX(S/T): 2

MRLP RRA ALGLLPLLLL PPAPEAKKPTPCHRCRGLV DKF NQGMVDTAKKNF GGGNTAWE EKTL SKYESSEIRL
LEILEG LCESSDFECNQMLEAQEEHLEA WNLQLKSE YPD LFEW PCV TLK VCCSPG TYGP DCLAC QGG SQR P CSG
NGH CSGD GS RQGD GS CRCH MG YQGP LCTDCMDG YFSSLRNE THS I CTAC DESCKT CSGL TNR DCGEV GWV LDE
GAC VD VD ECA A EPP PC SAA QF CKNANG SYT CEE CDS SCV GCT GEG PGN CKE C ISGY ARE H GQ CAD VDE C S L A EKT
CVR KNEN CYNTPGS YVCVCPDGF EETE D ACVPPA EAE TE GESPT QLPS RDL

Signal peptide:

amino acids 1-24

N-glycosylation sites.

amino acids 190-194 and 251-255

Glycosaminoglycan attachment sites.

amino acids 149-153 and 155-159

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 26-30

Casein kinase II phosphorylation sites.

amino acids 58-62, 66-70, 86-90, 197-201, 210-214, 255-259, 295-299, 339-343
and 349-353

Tyrosine kinase phosphorylation site.

amino acids 303-310

N-myristoylation sites.

amino acids 44-50, 54-60, 55-61, 81-87, 150-156, 158-164, 164-170, 252-258 and
313-319

Aspartic acid and asparagine hydroxylation site.

amino acids 308-320

EGF-like domain cysteine pattern signature.

amino acids 166-178

Leucine zipper pattern.

amino acids 94-116

TYDQDZG - S5T92D0660

FIGURE 3

CAGGTCCAAC TG CACCT CG GT TCTAT CG ATT GAA TCCC CGGG GAT CCT CTAG AGAT CCC TC
GACCT CG ACCCA CG CGT CC CG CAGG CG GAGG CG AC GCG CC CAG CG CT TA AAC CGG AA CA
GCC CT GG CT AGGG AGG CT GCG CG CAG CAG AGT AT CT GAC CG CG CC AG GT TG CT AGG TG CG
GC AC GAGG AG TTT CG CG CAG CG AGG AGG TCT GAG CAG CAG **AT** GG CCG GAG GAG CG CC TT C
CCT GCG CG CG CT CG CG AGG AT CCT CT CG CT GT GCG CT GG CA CT GCG CG GAG GC
CGGG CG CG CG CAG GAGG AGG AGG TCT GAC GAT CG AT GCT CAC CAG GCA AG AG TACT CA
TAGG AT TGA AGA AGA AT TCT GATT GT TT CAG AGGG GAA AT GG CAC CT TTA AC AT GAT
TT CAG AAA AG CG CA AC AGA AT GCG AG T TCT GT CT GCA T AT CCT CA TCC AT G A TTT AC
CT GCG CA AG CT GCG CAG GAG CAG A ACT AT CT TCT GCT GCG CT CC GT GATA
AAGG C AT CG CG CAG AT CCA AC CG TCA AT GT CCT CT GCG GAA CGT GCG CT CAC AAG CG CA
TCAG TT GT CA AG GT TGT GGT TCC AT GT CT GG AAA AC AGG AT GGG GT GG CAG CATT G A AGT
GG AT GT GAT GT GT TGA AGG CA AC CAC ATT CT CAA AC CAC CT CAA AT GCT AT CT
TC TTT TAA AAC AT GT CA ACA AC AGT CG AT GCT CG CC AGGG GT GT CG CAA AT GG AGG CTT GT AAT
GAA AG AC G C AT CT GCG AGT GT C TGT AT GGG TT CC AC GG AC CT C ACT GT GAG AAG CC TT G
TAC CC CAC G AT GT AT GA AT GT GT GG A CTT GT GT GACT CT GCT GT GAT CT GCC C A CT G
GAT T T AT GT GG AGT GA AT CT GT GCA AA AG CAA ACT GT C TCA AC C C T GCT TTA AT GG AGG GAC C
TG TTT CT ACC CT GG AAA AT GT TAT TGT CCT CC CAG GACT AG AGG GAG AG CAG TGT GAA AT CAG
CAA AT GCC CCA AC CC CT GT CGA AT GG AGT TAA AT G CATT GT G TAA AG CAA AT GT AAG TGT
CC AA AG GT TAC CG GAG GAG AC CT GT TCA AA GCG CT GT CG GAG GCT GT GG GT GAC AT
GGA AC CT GCG CAT GA ACC CAA AT GT C TCA AGA AG GT TGG C AT GG AAG AC ACT G CAA
TAA AAG GT TAC G AAG CG CAG CCT CATA C AT GCG CT GAGG C CAG CAGG G C CAG CT CAG G CAG
AC AC CG CT TCA CTT AAA AGG CG GAG GAG CG CG GG GAT CC AC CT GT AAGT CCA AT TAC AT CT GG
TG AACT CG CAC AT CT GAA AC CG TTT TA AGT TAC ACCA AGT TCA TAG CTT GT TAA CCT TCA
TG TGT GAA GT GT CAA AAT AT GT TCA TT AC CTT AAG AAT ACT GCG CT G AAT TTT AT TGT
TC ATT TAA AT CACT GAG CT GAT AT TTA AT CTT CTT TA AGT TTT CT AAG TAC GT CT GT TAG
CAT GAT GT TAT AG AT TT CTT GT TGT CAG TGT GAG AT GCG AGA TTT TAT AT GT CA ATT G A
TCAG GT TAA AT TT CTT CAG TGT GAG AT GCG AGA TTT TCA AAT CAC AT G CATT TAT GT
GT CT GGG G CAG G G A AC AT CAG AA AG GT TAA AT GGG CAA AA AT CG GT AAG T CAC AAG AAT
TT GG AT GT GT CG AG TTA AT GT GT GAG GT TA CAG CATT TCA G AAT TT TAT GT CAG AT ATT TGT
GTT TGT TCA ATT TTT AAA AAT GT CT TTA ATT TTT AA ACT CT CA AT CAA AT AT ATT TT GACC
TT ACC CATT ATT CC CAG AG A TCT CAG TATT AAA
AA A C A A T A A T A A T A T T C T A A C A C A T G A A A T A C G G A A T A A T G T A T G A A C T T T T G C A T
TGG CTT G A G C A A T A A T A A T A T T G T A A A C A A A A C A G C T C T T A C C T A A T A A C A T T T T A T
A C T G T T G T A T G T A A A A T A A A G G G C G C C G G A C T C T A G A G T C G A C C T G C A G A A G C T T G G C
CGCC AT GG C C C A A T T G T T A T T G C A G C T T A A T G T

FIGURE 4

TOP/ID: 552010

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA33094
><subunit 1 of 1, 379 aa, 0 stop
><MW: 41528, pI: 7.97, NX(S/T): 2
MARRSAFPAAALWLSSILLCLLALRAEAGPPQEESLYLWIDAHQARVLIGFEEDILIVSEGK
MAPFTHDFRKAQQRMPAIPVNIHSMNFTWQAAGQAEYFYEFSLRSLDKGIMADPTVNVPLL
GTVPHKASVVQVGFPCLGKQDGVAAFEVDVIVMNSEGNTILQTPQNAIFFKTCQQAECPGGC
RNNGFCNERRICECPDGFHGPCKEAKALCTPRCMNGGLCVTPGFCICPPGFYGVNCDAKANCST
TCFNGGTCFPYPGKCICPPGLEGEQCEISKCPQPCRNGGKICGKSKCKCSKGYQGDLCSPVC
EPGCGAHGTCHEPNKCQCQEGWHGRHCNKRYEASLIHALRPAGAQLRQHTPSLKKAEERRDP
PESNYIW

Signal peptide:

amino acids 1-28

N-glycosylation site.

amino acids 88-92, 245-249

Casein kinase II phosphorylation site.

amino acids 319-323

Tyrosine kinase phosphorylation site.

amino acids 370-378

N-myristoylation sites.

amino acids 184-190, 185-191, 189-195, 315-321

ATP/GTP-binding site motif A (P-loop).

amino acids 285-293

EGF-like domain cysteine pattern signature.

amino acids 198-210, 230-242, 262-274, 294-306, 326-338

FIGURE 5

CGGACGCGTGGGCGTCGGCGGTCAGAGCCAGGAGGGCGAGGGCCAGGGCTGGGCCCCACGGCTGGG
CCCCAGCCCCACACCTTCACACAGGGCCAGGGCACC **ATG**TGGCGATGTCCTGGGCTAC
TGTCTGTTGCTGCCGCTGGCTGGCACTTGGCTCTGGGTCGCCAGCAGGGCTGTGGGCGCCG
GAGCTAGCACCGGGCTGCACCTGCGGGCATCCGGACGCGGGAGGGCGGTACTGCAGGA
GCAGGACCTGTGCTGCCGGGGCGTGGCCAGCAGACTGTGCCCCCTGCCCTACCTGGGCGCAGCT
GTTACTGTGACCTCTCTGCACCGCAGGTCTCCGACTGCTGCCCTGACTTCTGGGACTTC
TGCCCTGGCGTGCCACCCCCCTTCCCCCGATCCAAGGGATGTATGCATGGAGGTGATCTA
TCCAGTCTTGGGAACGTACTGGGACAACCTGTAACCGTTGACACCTGCCAGGAGAACAGGCAGT
GGCATGGTGGATCCAGACATGATCAAAAGCATCAACAGGGCAACTATGGCTGGCAGGCTGG
GAACCCACAGGCCCTCTGGGCATGACCTGGAT**TAGGGG**CATTGCTACGCCCTGGCACC
TCCGCCCATTTCTCGTCATGAACTGATGAAATTTATAAGTGTGTAACCCAGGGAG
GTGCTTCCCACAGCGGCTCGAGGCTCTGAGAAGTGGCCACCTGATTCACTGAGCCTTGTGA
CCAAGGCAACTGTGAGGCTCTGGGCTCTCCACAGCAGCTGTGCATCCGATCTGTCT
CAATCCATTCTCTGGACACATGACGCCCTGCTCTGTCGCCCAAGAACCTGCTGTCTTGTAC
ACCCAGGACAGCAGGGCTGGGCTGGGCTGGGCTGGGATGGTGGCTGGGTTCTGGCTCG
CCGAGGGTGGTGTGACACTGCTACCCCTTCTGGGCTGGGCAAGGCCAGGCCACTGCC
CTGGCCCCCTGTATGATGACAGGCCATGGTCGGGCAAGGCCAGGCCACTGCC
CACTGCCCAACACAGCTATGTTAAATACATGACATCTGGAGGTACTCTGTCACCC
CGGCTTCAACAGACAAGGAGATCATGAGGGAGCTGATGGAGAATGGCCCTGTCCAAGGCC
TGGAGGTGATGAGGACTTCTTCTTATAACAGGGAGGCACTCAAGGAGATCACAGGATGGGG
CTTGGAGGGCCAGAGAGATAACCCCGGCTGGGACCCACTCAAGGAGATCACAGGATGGGG
AGAGGAGACCTGCGAGATGGAGGACCTGCAAAATACTGGACTGGGCAACTCTGGGGCC
CAGCCTGGGGAGAGGGGCCACTTCCGCACTCGCCTGGCTCAATGAGTGCACATCGAG
AGCTTCTGTGCTGGGCGTCTGGGCGCTGGGCGTGGGATGGAGGACATGGGTCTACTGAGGCTG
CGGGCACCCACGGCTGGGCGTGGGCGTGGGATCCAGGCTAAAGGGCGGGGAGAGGGCCCAATG
GGGCGGTGACCCAGCCTCGCCCGACAGAGCCGGGGCGCAGGGGGCCAGGGCGTAAAT
CCCGCGCGGGTTCCGCTGACGCGAGGCCCTGGGAGGCCGGCAGGGAGACTGGG
GAGCCCCAGACCTCCAGTGGGAGCGGGCAGGGCTGGCTGGGAAGAGCACAGCTGCAG
ATCCCAGGCCCTGGGCCCTTCAAGACTACAAAGGCCAGGACACCTCAAGTCTCCAGC
CCCAATACCCACCCCAATCCGTATTCTTTTTTTTTAGACAGGGCTTGCTCC
TTGCCAGGGTGGAGTGCAGTGCCCCATCAGGGCTCACTGTAACCTCCGACTCTGGGTTCA
AGTGAACCCCTCCACCTCAGGCTCAAGTAGCTGGGACTACAGGTGACCCACACACTGGC
TAATTTTTGTATTTTTGTAAAGGGGGGCTCACTGTGTTGCCAGGCTGGTTCAACT
CCTGGGCTCAAGCGGTCCACCTGCCTCCGCTCCAAAGTGTGGGATTGCAGGCATGAGCC
ACTGCACCCAGCCCTGTATTCTTATTCTCAGATATTATTTCTTTCACTGTTTAA
TAAACCAAAGTATTGATAAAAAAAA

FIGURE 6

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA33223
><subunit 1 of 1, 164 aa, 1 stop
><MW: 18359, pI: 7.45, NX(S/T): 1
MWRCPLGLLLLLPLAGHLALGAQQGRGRRELAPGLHLRGIRDAAGGRYCQEQLLCRGRADDC
ALPYLGAICYCDLFCNRVSDCCPDFCLGVPPFPPIQGCMHGGRIYPVLGTYWDNCNR
CTCQENRQWHGGSRHDQSHQPGQLWLAGWEQRLLGHDPG

N-glycosylation site.

amino acids 78-82, 161-165

Casein kinase II phosphorylation site.

amino acids 80-84, 117-121, 126-130, 169-173, 205-209, 296-300,
411-415

N-myristoylation site.

amino acids 21-27, 39-45, 44-50, 104-110, 160-164, 224-230,
269-275, 378-384, 442-448

Amidation site.

amino acids 26-30, 318-322

Eukaryotic thiol (cysteine) proteases histidine active site.

amino acids 398-409

YD007200-5T92020660

FIGURE 7

AGGCTCCTGGCCCTTTCCACAGCAAGCTTNTGCNATCCGATTGTTGTCCTCAAATCCA
ATTCTCTGGACACATNACGCCTGCTTNGCCCCAGAACCTGCTGCTGTACACCCAC
CAGCAGCAGGGCTGCCCGNTGGCGTCTCGATGGTGCCTGGTGGTTCTGCGTCGCCGAGG
GNTGGTGTCTGACCCTGCTACCCCTCTCGGGCGTGAAACGAGACGAGGCTGGCCCTGCGC
CCCCCTGTATGATGCACAGCCGAGCCATGGGTGGGCAAAGCGCCAGGCCACTGCCACTGC
CCCAACAGCTATGTTAATAACAATGACATCTACCAGGTCACTCCTGTCACCGCCTGGCTC
CAAAGACAAGGAGATCATGAAGGAGCTGATGGAGAATGCCCTGTCAGCCACAGCCAGTGAGCCTGGG
TGCAATGAGGACTTCTTCTTACAGGGAGGCATCTACAGCCACAGCCAGTGAGCCTGGG
AGGCCAGAGAGATAACGCCGGCATGGACCCACTCAG

FIGURE 8

GCTGCTTGCCTGTTGATGGCAGGCTTGGCCCTGCAGCCAGGCAGTGCCTGCTGTGCTACT
CCTGCAAAGCCCAGGTGAGCAACGAGGACTGCCTGCAGGTGGAGAAGTGCACCCAGCTGGGG
GAGCAGTGCTGGACCGCGCAGTCCGGCGAGTTGGCCTCTGACCGTCATCAGCAAAGGCTG
CAGCTTGAACGTGGATGACTCACAGGACTACTACGTGGCAAGAAGAACATCACGTGCT
GTGACACCGACTTGTGCAACGCCAGCGGGGCCATGCCCTGCAGCCGGCTGCCGCATCCTT
GCGCTGCTCCCTGCACCGCCTGCTGCTCTGGGACCCGGCCAGCTATAAGGCTCTGGGGGG
CCCCGCTGAGCCACACTGGGTGTGGTGGCCAGGCCCTGTGCCACTCCTCACAGACCTG
GCCAGTGAGGAGCCTGCTGGTCCCTGAGGCACATCCTAACGCAAGTCTGACCATGTATGT
CTGCACCCCTGCCCCCACCTGACCCCTCATGGCCCTCTCCAGGACTCCCACCCGGCAGA
TCAGCTCTAGTGACACAGATCCGCCTGCAGATGGCCCTCCAACCCCTCTGCTGCTGTTTC
CATGGCCAGCATTCTCACCCCTAACCTGTGCTCAGGCACCTCTTCCCCAGGAAGCCTT
CCCTGCCACCCCATCTATGACTTGAGCCAGGTCTGGTCCGTGGTGTCCCCGACCCAGCA
GGGGACAGGCACTCAGGAGGGCCAGTAAAGGCTGAGATGAAGTGGACTGAGTAGAACCTGGA
GGACAAGAGTCGACGTGAGTTCTGGAGTCTCCAGAGATGGGCCCTGGAGGCCTGGAGGAA
GGGCCAGGCCACATTGGGGCTCCCTGAATGGCAGCCTGAGCACAGCGTAGGCCCTT
AATAAACACCTGTTGGATAAGCCAAAAAA

FIGURE 9

MTHRTTTWARRTSRAVTPCATPAGPMPCSRLPPSLRCSLHSACCSGDPASYRLWGAPLQPT
LGVVPQASVPLLTDLAQWEPVLVPEAHPNASLTMYVCTPVPHPDPPMALSRTPTRQISSLDT
DPPADGPSNPLCCCFHGPAGFSTLNPVLRHLFPQEAFPAHPIYDLSQVWSVSPAPSRGQALRRAQ

Signal peptide:

amino acids 1-47

N-glycosylation site.

amino acids 31-35, 74-78, 84-88

Casein kinase II phosphorylation site.

amino acids 22-26, 76-80

N-myristoylation site.

amino acids 56-60

Amidation site.

amino acids 70-74

09092015-1371001

FIGURE 10

CCCCACGCGTCCGAACCTCTCCAGCGATGGGAGCCGCCCTGCTGCCAACCTCACTCTGT
GCTTACAGCTGCTGATTCTCTGCTGTCAAACCTCAGTACGTGAGGGACCAGGGCGCCATGACC
GACCAGCTGAGCAGGGCAGATCCGCGAGTACCAACTCTACAGCAGGACCAGTGGCAAGCA
CGTGCAGGTACCGGGCGTCGCATCTCCGCCACCGCCGAGGACGGCAACAAGTTGCCAAGC
TCATAGTGGAGACGGACACGTTGGCAGCCGGTTGCGATCAAAGGGCTGAGAGTGAGAAG
TACATCTGTATGAACAAGAGGGCAAGCTCATCGGGAAAGCCCAGCGGAAGAGCAAAGACTG
CGTGTTCAGGGAGATCGTGTGGAGAACAACTATAACGCCCTTCAGAACGCCCGCACGAGG
GCTGGTTCATGGCTTCACGGCGAGGGCGGCCCGAGGCTTCCCGCAGCCGCAAGAAC
CAGCGCGAGGCCACTTCATCAAGGCCCTACCAAGGGCAGCTGCCCTCCCCAACACGC
CGAGAACGAGCAGTCAGTTGAGTTGTGGCTCGCCCCCACCGCCGACCAAGCGCACAC
GGCGGCCCTAGCCCCTCACGTAGCTGGAGGGAGGGCGAGCACCCCTGGCCGCTCCC
CACCCCTTCCCTTAACTCAAGGACTGGCTGGGCTGGCGGGAGGGAGCCAGATCCCC
GAGGGAGGACCCCTGAGGGCGCGAAGCATCCGAGCCCCCAGCTGGAAAGGGGCAGGCCGGTG
CCCCAGGGCGGCTGGCACAGTGCCCCCTTCCGGACGGGTGGCAGGCCCTGGAGAGGAAC
GAGTGTACCCCTGATCTCAGGCCACAGCCTCTGCCGGCTCCAGCCGGCTCTGAAGCC
CGCTGAAAGGTCAAGCGACTGAAGGCCCTGCAAGACAACCGCTGAGGGCTGTCTCAA
TCTGCTTCTCGGATCTCCCTCAGTCTGCCCTCAGGCCCTAGCCCCAAACTCCTCCTGGCTAGACTGTA
GGAAGGGACTTTGTTGTTGTTGTTCAAGGAAAAAGAAAGGGAGAGAGAGGAAATAG
AGGGTTGTCACTCCTCACATTCCACGACCCAGGCCTGCACCCCAACTCCAGCCC
CGGAATAAAACCATTTCCTGC

FIGURE 11

MGAARLLPNLTLCLQLLILCCQTQYVRDQGAMTDQLSRRQIREYQLYSRTSGKHVQVTGRRI
SATAEDGNKFAKLIVETDTFGSRVRIKGAESEKYICMNKRGKLIGKPGSKSKDCVFTIEIVLE
NNYTAQNARHEGWFMAFTRQGRPRQASRSRQNQREAHFIKRLYQGQLPFPNHAEKQQQFEF
VGSAPTRRTKRTTRPQPLT

Signal peptide:

amino acids 1-22

N-glycosylation site.

amino acids 9-13, 126-130

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 60-64

Casein kinase II phosphorylation site.

amino acids 65-69

Tyrosine kinase phosphorylation site.

amino acids 39-48, 89-97

N-myristoylation site.

amino acids 69-75, 188-194

Amidation site.

amino acids 58-62

HBGF/FGF family signature.

amino acids 103-128

FIGURE 12

ACCTGGCCATCACCTGGTGGCCAGTGTGGAAAAAATTCTCCCTGTTGAATTTCGCACATGGAG
GACAGCAGAAAGGGCAACAGGCTGATAAGACAGAGACAGCAGGGAGATTATTTCAC
CATACGCCCTCAGGACGTTCCCTAGCTGGAGTTCTGGACTTCACAGAACCCATCCAGT
CATTTTGATTGTTGCTGTTATTTTTCTTTCTTCCACACATTGTATTTCAT
TTCGGTACTTCAGAAATGGGCTTACAGACCAAAAGTCCGCACCCATGGGCTTTTCT
GAAGTCTGGCTTATCATTCCCTGGGGCTACTCACAGGTGTCACAACTCTGGCTGCC
CTAGTGTGTCGCGCTGCGACAGGAACCTTGCTACTGTAATGAGCGAAGCTGACCTCAGTG
CCTCTGGGATCCCGAGGGCTAACGGTACTCTACCTCCACAAACAACCAAAATTAAATG
TGAGTTTCTGCGAGAACTGCAATGTACAGTGGTGCACACGGCTACCTGTATGGCAACC
AACTGGACGAATTCCCCATGAACCTTCCAGAAATGTCAAGAGTTCTCCATTGCGAGAAAAC
AAATATTCAAGACCATTTCACGGGCTGCTTGTGCCCAGCTTGAGCTGAAGAGCTGCACCT
GGATGACAACCTCCATATCCACAGTGGGGTGGAAAGCAGGGCTTCCGGGAGGCTATTAGCC
TCAAAATGTTGTTTGTCTAAAGATCACCTGAGCAGTGTGCTTGTGGGCTTCTGTGGAC
TTGCAAGAGCTGAGAGTGGATGAAAATCGAATTGCTGTATATCGACATGGCTTCAGAA
TCTCACAGAGCTGGAGCTTATGTGGACGGGAACTCTGTGACCAACAAGGGTATCGCC
AGGGCACCTTCAGCATCTCAACAGCTCAAGGAATTTCATTGTACGTAATTGCTGTCC
CACCCCTCTCCCGATCTCCAGTACGCTCTGATCACGGCTCTATTGCGAGAACCCAGAT
AAACACACATTCTTGTACAGCCTCTCAAACTTCGCTGAAGCTGGAACGGCTGGATATATCCA
AAACACACTGGGATGCTGACTCAAGGGTTTGTATAATCTCCACACCTGTGACGAGCTC
ACTGCTCGAATAACCCCTGGTTTGTACTGCTGAGTAAATGGGTACAGAATGGCTCAA
ATATATCCTTCATCTCAACGTGCGGGTTTGTGCAAGGTCTGACAAAGTCCGGG
GGATGGCGCTCAGGGAAATTAAATGTAAATTGCTTGTCTGCCACAGGACCCCCGGCTG
CTCTCTTCACCCCGACAGTACAGCTTCTCCGACACTCAGCTCCACCCCTCTCAT
TCCAAACCCTAGCAGAAGCTACAGCCTCCAACTCTTACACATCGAAACTTCCCAGATT
CTGACTGGGATGGAGAAAGAGTGGACCCCAACTTCTGACAGGATCCAGGCTCTCATC
ATATGTGAAATGATACTTCAAGTCAGCTGGCTCTCTCTTACCGTGTGACGGATA
CAAACCTCATGGGTGAAATGGCCACAGTTAGTGGGGCATCTTCAGGAGCGCATAG
TCAGCGGTGAGAAGCAACACCTGAGCCTGTTAACCTAGAGCCCCGATCCACCTATCGGATT
TGTGTTAGTGCCTACTGGATGCTTTAACTACCGCCGGTAGAAGACACCATTTGTTCAAGGGC
CACCAACCCATGCCCTATCTGAAACAGGCGACGAAACACAGCTCCAGCATGAGCACAGA
CGTCCCACAGCATGGCTCCCTTTCTGCTGGGGCTGTGATGGGGCGGGTGTATTT
GTGCTGGTGCTTGCTCAGCGTTTGTGCTGGCATATGACACAAAAGGGGCGCTACACCTC
CCAGAAGTGGAAATACAACCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG
AGGACAACTCCATCTGGAGATGACAGAAACAGTTTACAGATGTCCTTAAATAACGAT
CAACTCTTAAAGGAGATTTGAGACTGCAAGCCATTACACCCAAATGGGGCATTAATT
CACAGACTGCCATATCCCCAAACATGCGATACTGCAACAGCAGCGTGCAGACCTGGAGC
ACTGCCATACGTGACAGCCAGAGGCCCCAGGTATCAAGGCGACAATTAGACTCTTGAGAA
CACACTCGTGTGACATAAGACAGCAGATTACATTGATAAAATGTTACACAGATGCAT
TTGTGCATTGAAACTCTGTAATTATACGGTGTACTATATAATGGGATTAAAAAAAGTG
CTATTTCTATTCAAGTTAACACAGTTTGTAAACTCTTGTCTTTAAATCTT

FIGURE 13

MGLQTTKWPShGAFFLKSWLIIISLGLYSQVSKLLACPSVRCDRNFVYCNERSLTSVPLGIP
EGVTVLYLHNQINNAGFPAAELHNVQSVHTVYLVGNQLDEFPMNLPKNVRVLHLQENNIQTI
SRAALAQLLKLEELHLDDENSISTVGVEDGAFREAISSLKLLFLSKNHLSVPVGLPVDLQELR
VDENRIAVISDMAFQNLTSLERLIVDGNLITNKGIAEGTFSHLTKLKEFIVRNSLSHPPD
LPGTHLIRLYLQDNQINHIPLTAFSNLRKLERLDISNNQRLMLTQGVFDNLNSNLQLTARNN
PWVFCDCS1KVVTEWLKYIPLSSLNVRGFMCGPEQVRGMAMVRELNMNLSCPTTPGLPLFTP
APSTASPTTQPPTLSIPNPSRSYTPPTPTSKLPTIPDWDGRERVTPISERIQLSIHFVND
TSIQVSWLSSLFTVMAYKLTWVKMGHSLVGGIVQERIVSGEKQHLSLVNLEPRSTYRICLVPV
DAFNYRAVEDTICSEATTHASYLNNNGNTASSHEQTTSHSMGSPFLLAGLIGGAVIFVLVVL
LSVFCWHMHKKGRYTSQKWKYNRRRKDDYCEAGTKKDNSILEMTETSFQIVSLNNNDQLLKG
DFRLQPIYTPNGGINYTDCHIPNNMRYCNSSVPDLEHCHT

Signal peptide:

amino acids 1-42

Transmembrane domain:

amino acids 542-561

N-glycosylation site.

amino acids 202-206, 298-302, 433-437, 521-525, 635-639, 649-653

Casein kinase II phosphorylation site.

amino acids 204-208, 407-411, 527-531, 593-597, 598-602, 651-655

Tyrosine kinase phosphorylation site.

amino acids 319-328

N-myristoylation site.

amino acids 2-8, 60-66, 149-155, 213-219, 220-226, 294-300,
522-528, 545-551, 633-639

Amidation site.

amino acids 581-585

Leucine zipper pattern.

amino acids 164-186

Phospholipase A2 aspartic acid active site.

amino acids 39-50

FIGURE 14

FIGURE 15

MEKMLAGCFLLILGQIVLPLAEARERSRGRSISRGRHRARTHPTQTALESSCENKRADLVFII
DSSRSVNTHDYAKVKEFIVDILQFLDIGPDVTRVGLLQVGSTVKNEFSLKTFKRKSEVERAV
KMRMRHLSGTGTMGLAIQYALNIAFSEAE GARPLR ENVPRVIMIVTDGRPQDSVAEVAAKARD
TGILILFAIGVGQVDFN T LK SIGSEPHEDHVFVLVANFSQIETLTSVFOKKLCTAHMCSTLEHN
CAHFCINI PGSYVCRCKQGYILNSDQTT CRIQDLCAMEDHNC EQLCVNVPGSFVCQCYSGYA
LAEDGKRCVADVYCASENHGCEHECVNADGSYLCQC HEGFALNPDEKTCTRINYCALNKPGC
EHECVNMEESYYCRCHRGYTLDPNGKTC SRVDHCAQQDHGCEQLCLNTEDSFVCQCSEGFLI
NEDLTKTCSRVDYCLLSDHGEYSCVNMDRSFACQCPEGHVLRS DGKTCAKLDSCALGDHGCE
HSCVSSEDSFVCQCPEGYILR EDGKTCR RDV CQAIDHGCEHICVNSDDS YTCECLEGFRLA
EDGKRCR RDV C KST H HGCEHICVNNNGNSYI C K CSEG FV LAEDGRRCKKCTEGPIDLVFVID
GSKSLGEENFVVVKQFVTGII D SLT I SPKAARVGLLQYSTQVHTEFTL RNFNSAKDMKKAVA
HMKYMGKGSMTGLALKHMFERSFACQCPEGHVLRS DGKTCAKLDSCALGDHGCE
GITMYAVGVGKAIEELQEIASEPTNKHLYFAEDFSTMDEI SEKLKKGICAELEDSDGRQDS
PAGELPKTVQQPTESEPVTINI Q DLLCSN FAVQHRYLFEEDNLLRSTQKL SHSTKPSGSPL
EKEHDQCKCENLIMFQNLANEEVRKLTQRL EEMTQRMEALENRLR YR

Signal peptide:

amino acids 1-23

N-glycosylation site.

amino acids 221-225

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 115-119, 606-610, 892-896

Casein kinase II phosphorylation site.

amino acids 49-53, 118-122, 149-153, 176-180, 223-227, 243-247, 401-405, 442-446, 501-505, 624-628, 673-677, 706-710, 780-784, 781-785, 819-823, 866-870

N-myristoylation site.

amino acids 133-139, 258-264, 299-305, 340-346, 453-459, 494-500, 639-645, 690-696, 752-758, 792-798

Amidation site.

amino acids 314-318, 560-564, 601-605

Aspartic acid and asparagine hydroxylation site.

amino acids 253-265, 294-306, 335-347, 376-388, 417-423, 458-464, 540-546, 581-587

FIGURE 16

GGAGCCGCCCTGGGTGTCAGGGCTGGCTCCCGCGCACGCTCCGGCGTCGCAGCCTCG
GCACCTGCAGGCCGTGCGTCCCGCGCTGGCGCCCTGACTCCGTCCGGCCAGGGAGGGC
CATGATTTCCCTCCGGGCCCTGGTACCAACTTGCTGCGGTTTTGTTCCCTGGGTGA
GTGCCCTCGGCCCTCGCGGCCAGCTGCAACTGCACTTGCCCCCAACGGGTGAG
GGGGTGGAGGGAGGGGAAGTGGTGCTTCCAGCGTGGTACACCTTGACAGGGAGGTGCTTC
ATCCCAAGCCATGGGAGGTGCCCTTGTGATGTGGTTCTCAACAGAAAGAAAAGGAGGATC
AGGTGTTGTCATCATCAATGGGGTACAACAAGCAAACCTGGAGTATCCTGGTCTACTCC
ATGCCCTCCCGAACCTGTCCTGCGGCTGGAGGTCTCCAGGAGAAAGACTCTGGCCCTA
CAGCTCGTCCGGAATGTGCAAGACAAACAAGGAAATCTAGGGCCACGCATAAAACCT
TAGAACTCAATGTAATGGTCCAGCTCCATCTGCGTCTCAGGGTGTGCCCAT
GTGGGGCAAACTGACCCCTGAGCTGCCAGTCTCAAGGAGTAAGCCGCTGTCCAATACCA
GTGGGATCGGCAGCTCCATCTCCAGACTTCTTGACCCAGCATTAGATGTCATCCGTG
GGTCTTAAGGCTACCAACCTTCTGCTCTCCATGGCTGGAGTCTATGTCAGGCCAC
AATGAGGTGGCACTGCCAATGTAATGTCAGCTGGAGTGGACAGCAGGGCTGGAGCTGC
AGTGGTTGCTGGAGCTGTTGCTGGTACCTGGTTGGACTGGGTTGCTGGCTGGCTGGTCC
TCTTGTAACCCGCCGGGCAAGGCCCTGGAGGAGGCCAGCAATGATATCAAGGAGGATGCC
ATTGCTCCCCGGACCCCTGCCCTGGCCAAGAGCTCAGACACAATCTCCAAGAATGGGACCT
TTCCTCTGTCACTCCGCACGCCCTCCGGCACCCATGGCCCTCCAGGGCTGGTGCAT
TGACCCCCACGCCAGTCTCCAGGCCAGGCCCTGCCCTCACCAAGACTGCCACGACAGAT
GGGGCCACCTCAACCAATATCCCCCATCCCTGGGGTTCTCTCTGGCTTGAGCCG
CATGGGTGCTGCTGTGCTGTGATGGTGCCTGCCAGAGTCAGACTGGCTCTGGTAT**GATGAC**
CCCACCACTCATGGCTAAAGGATTGGGCTCTCCTCTATAAGGGTACCTCTAGCAC
AGAGGCCCTGAGTCATGGGAAAGAGTCACACTCTGACCTTAGTACTCTGCCCACTCTC
TTTACTGTGGAAAACCATCTCAGTAAGACCTAAGTGTCCAGGAGACAGAAGGAGAAGGAGA
AGTGGATCTGGAATTGGGAGGAGCCTCCACCCACCCCTGACTCTCTTATGAAGGCCAGCTG
CTGAAATTAGCTACTCACCAAGAGTGAGGGCAGAGACTTCCAGTCAGTCACTGAGTCTCCAGGC
CCCCCTGATCTGTACCCACCCCTATCTAACACCACCCCTGGCTCCACTCCAGCTCCCTGT
ATTGATATAACCTGTCAGGCTGGCTTGGTTAGGTTTACTGGGGCAGAGGATAGGAATCTC
TTATTAACATGAAATATGTTGTTTCAATTGCAATTAAAGATACTAA
TGTTGTATGAAAAA

FIGURE 17

MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHL PANRLQAVEGGEVVLPAWYTLHGEVSS
SQPWEVPFVMWFFKQKEKDQVLSYINGVTTSKPGVSLVYSMPSRNLSLRLEGHQEKDGPY
SCSVNVQDKQGKSRGHSIKTLELNVLVPPAPPSCRLQGVPHVGANVTLSQSPRSKPAVQYQ
WDRQLPSFQTFFAPALDVIRGSLSLTNLSSSMAGVYVCKAHNEVGTAQCNVTLEVSTGPGAA
VVAGAVVGTTLVGLGLLAGLVLLYHRRGKALEEPANDIKEADAIAPRTLPWPKSSDTISKNGTL
SSVTSARALRPPHGPPPRPGALTPPSLSSQALPSRPLPTTDGAHPQPISPIPGGVSSSGLSR
MGAAPVPMVPAQSQAGSLV

Signal peptide:

amino acids 1-29

Transmembrane domain:

amino acids 245-267

N-glycosylation site.

amino acids 108-112, 169-173, 213-217, 236-240, 307-311

N-myristoylation site.

amino acids 90-96, 167-173, 220-226, 231-237, 252-258, 256-262,
262-268, 308-314, 363-369, 364-370

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 164-175

FIGURE 18

CGCCCCACTGGGCCACCCCAATGAAACGCCCTCCCTAGTGGTTTTCCACTTTG
TTGAATTGTTCTATACTCAAAATTGACCAAGACCTTGTCTCCAAATGCAAATGTGA
AATACGAATGGAATTGACGCTGCTATTGCAACATGGATTTCAGGAAATGGTGTCAAA
TTTGTGAAAGATGATAATGAAATGGAAATTAACTCAGTCTGTGGCGAAATGCTAATTG
ACTAACACAGAAGGAAGTTATTGTGTTGACCTGGCTTCAGATCCAGCAGTAACCA
AGACAGGTTTATCACTAATGATGGAACCGCTGTAGTAAAGAAATGTGAATGCAAATG
TAGATAATGCTGTATAGCTGCAAATATTAAATAAAACTTAAACAAAATCAGATCCATAAA
GAACCTGTGGCTTGTCTACAAAGAGTCATAGAAATTCTGTGACAGATCTTCACCAACAGA
TATAATTACATATAAGAAATTAGCTGAACTCTTACTAGGTTACAAGAACAAACA
CTATCTCAGCCAGGACACCCCTTCACTCAACTCTTACTGAATTGTAACAAACCGTGAAT
AATTGTTCAAAGGGATACTTGTAGTTGGGACAAGTTATCTGTGAATCATAGGAGAAC
ACATCTCACAACACTCATGACACTGTGAAACAGCTACTTTAAGGATATCCCAGAGCTTCC
AAAAGACACAGAGTTGATCAAATTCACGGATATAGCTCTCAAAGTTTCTTTTGAT
TCATATAACATGAAACATATTCTATCCTCATATGAATATGGATGGAGACTACATAAATATATT
AGAGATAATGGTCTTGTCTCATCTGACAACCTTCTATTGAAACCTCAAAATTATGAT
AATTCTGAAGAGGAGAAAGTCTATCTTCACTGAACTTCAATTCTAGTCATGAGCTCAAACCC
ACCCACATTATGAACTTGTGAAAATAACATTACATTAAGTCTACAGGTCACAGATA
GGTATAGGGACTATGTGCTTTGGAAATTACTCACCTGATACCATGAATGGCAGCTGGTCT
TCAGAGGGCTGTGAGCTACACTAATGAGACCCACACTCATGCCCTGTAATCACCT
GACACATTTCGAATTGATGTCCTGGCTCTCCATTGGTATTAAAGATTATAATTCT
TCAAAAGGATCACTCAACTAGGAAATAATTCTACTGATTGCTTGCATATGCAATT
ACCTCTGGTTCTCAGTGAACATTCAAAGCACCAGGACAACAATTCAAAAATCTTGTG
TAGCCTATTCTCTGCTGAACCTGTTTCTCTGGGATCAATACAATAACTAAAGCTCT
TCTGTTCAATCATTGCCGACTGCTACACTACTTCTTTAGCTGCTTTGCATGGATGTG
ATTGAGGCAATACATCTCATCTCATGGTGGGTGATCTACAAACAGGGATTGGCA
CAAGAATTTTATATCTTGGCTATCTAAGGCCAGCGCTGGTAGTTGGATTTCGGCAC
TAGGATAACAGATATTGGACAACCAAAAGTATGGCTTAGCACCACAACTTTATT
TGGGATTTTATAGGACAGCATGGCTAACTCATTCTCTTAACTCTTGGCTTTGGAGTCAT
CATATAACAAAGTTTCTGCTCAACTCGCAGGGTTGAACACAGAAGTTAGTTGCTTTG
TAAGGTCTGTGCAAGAGGGGCCCTGCTCTCTGTTCTCTCGGCCACACCTGGATCTT
GGGGTTCTCAGTGTGCAAGCAGCTACTGGTACAGCTTACCTCTCACAGTCAGGATGC
TTCCAGGGGATGTTCAATTCTCTGTTCTGTTCTAGAAAGATTCAAGAAGAAT
ATTACAGATTGTTCAAAATGTCCTCTGTTCTGGATGTTAAAGGTAAACATAGAAATG
GTGGATAATTACAACCTGCACAAAAAATAAAATCCAAAGCTGTGGATGACCAATGTATAAAA
TGACTCATAAATTCAAAATTAAACTACTAGACAAAAAGTATTAAATCAGTTTCT
GTTTATGCTATGAAACTGTAGATAATAAGGTTAAATTGTGATCATATAGATAACTATG
TTTCTATGAAATAGTTCTGTCAAAATAGTATGCAAGATATTGAAAGTAATTGTT
CTCAGGAGTGTATCACTGCACCCAAAGGAAAGATTCTTCTAACACGAGAAGTATATGAA
TGTCTGAAAGGAAACACTGGCTTGTGATTTCTGTGACTCTGTGTTGCTTTGAAACACTAGTCC
CCTACCCACCTCGCTAATGAGCTCCATTACAGGAAACTGGAAACATAAGAGAAATGAAAGGGCAGA
ATATCAAACAGTGAAGGGAAATGATAAGTGTATTGAAATGAAACTGTTTTCTGTG
TAGCTGAGAAATTGTTGACATAAAAGAATTGAAAGGAAACATTAACTTACCCATTGAA
TTGTTCTGAACTAAATGTCCTACTAAACACTTAGACTCTGTGTTGCTAAATCTGTTCTT
TTCTAATATTCTAAAAAAAGGTTACCTCCACAAATTGAAAGGAAAGGAAAGGAAAGGAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 19

MKRLPLLVVFSTLLNCSTQNCTKTPCLPNAKCEIRNGIEACYCNMGFSGNGVTICEDDNEC
GNLTQSCGENACTNTEGSYCMCVPGRSSNQDRFITNDGTVCIENVNANCHLDNVCAA
NINKTLTKIRSIKEPVALLQEVYRNSVTDLSPTDIITYIEILAESELLGYKNNTISAKDTL
SNTSLTEFVKTVNNFVQRDTFVWWDKLSVNHRRTHLTKLMHTVEQATLRIQSDFQKTTEFDT
NSTDIALKVFVFFDSYNMKHIIHFMNMDGDIYINIFPKRKAAVDNSGNVAVAFLYYKSIGPLLS
SSDNFLLKPONYDNSEEERVISSVISVMSNPTELVELEKITFTLSHRKVTDYRSLCAF
WNYS PDTMNGWSSEGCELTYSNETHTSCRNCNLTHFAILMSGPSIGIKDYNILTRITQLG
IIISLICLAI CIFTFWFFSEI QSTRITIHKNLCCSLFLAELVFLVGINTNTNKLFCSSIAGL
LHYFFLAFAWM CIEGIGHLYLIVVGVYIYNKGFLHKNFYIFGYLSPAVVVGFSAA LGYRYGT
TKVCWLSTENNF IWSFIGPACLIILVNLLA FG VVIIYKVFRHTAGLKPEVSCFENIRSCARGA
LALLFLLGTTWIFGVLVHVVASVVTAYLFTVSNAFQGMFIFLFLCVLSRKIQEEYYRLFKNV
PCCFGCLR

Signal peptide:

amino acids 1-19

Transmembrane domain:

amino acids 430-450, 465-486, 499-513, 535-549, 573-593, 619-636,
648-664

N-glycosylation site.

amino acids 15-19, 21-25, 64-68, 74-78, 127-131, 177-181,
188-192, 249-253, 381-385, 395-399

Glycosaminoglycan attachment site.

amino acids 49-53

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 360-364

Casein kinase II phosphorylation site.

amino acids 54-58, 68-72, 76-80, 94-98, 135-139, 150-154,
155-159, 161-165, 181-185, 190-194, 244-248, 310-314, 325-329,
346-350, 608-612

Tyrosine kinase phosphorylation site.

amino acids 36-44, 669-677, 670-678

N-myristoylation site.

amino acids 38-44, 50-56, 52-58, 80-86, 382-388, 388-394,
434-440, 480-486, 521-527

Aspartic acid and asparagine hydroxylation site.

amino acids 75-87

FIGURE 20

TGGAAACATATCCTCCCTCATATGAATATGGATGGAGACTACATAAATATTTCCAAAGNG
AAAAGCCGGCATATGGATTCAAATGGCAATGTTGCAGTTGCATTTTATATTATAAGAGTAT
TGGTCCCTTGCTTCATCATCTGACAACCTCTTATTGAAACCTCAAATTATGATAATTCT
GAAGAGCAGGAAAGAGTCATATCTTCAGTAATTCAGTCTCAATGAGCTCAAACCCACCCAC
ATTATATGAACCTTGAAAAAATAACATTTACATTAAGTCATCGAAAGGTACAGATAGGTATA
GGAGTCATGTGGCATTTGGAATACTCACCTGATACCATGAATGGCAGCTGGTCTTCAGAG
GGCTGTGAGCTGACATACTCAAATGAGACCCACACCTCATGCCGCTGAATCACCTGACACA
TTTGCAATTGATGTCCTCTGGCCTTCCATTGGTATTAAGATTATAATATTCTTACCAA
GGATCACTCAACTAGGAATAATTATTTCACTGATTTGTCTGCCATATGCATTTTACCTTC
TGGTTCTTCAGTGAAATTCAAAGCACCAGGA

FIGURE 21

GCTCCCAGCCAAGAACCTCGGGGCCGCTCGCGCGTGGGGAGGAGTTCCCGAAACCCGGCGG
CTAACGGAGGCCCTCCCTCCCGCAGATCGAACGGCTGGGGCGGGTCACCCGGCTGGGA
CAAGAACGCCGCCCTGCCCTGCCCTGCCGGGGGCCGGGGAGGGGGCTGGGGCTGGGGCGGAGGCCG
GGTGTAGTGGGTGTGCGGGGGCGGAGGGCTTGTGCAATCCCGATAAGAAATGTCGGG
TGTCTGGGCACCTACCCGTGGGGCCCGTJAAGGCCCTATATAAGGCTGCCGGGCCGGAG
CCGCCGGCCCGTCAAGAGCAGGCCGCTGCCCTCAGGATCTAGGGCACGCCACCCATGCCGG
GGCACTCACAGCCCCGAGCGCATCCCGTGCAGGCCAGCCTCCGCACCCCATGCCGG
AGCTGCGCCGAGAGGCCAGGGAGGTGCA**ATGCGGAGCGGGTGTGTGGTCCACGTATGG**
ATCCCTGGCGGCCCTGCCCTGCCCTGCCGCCCTCGCCTTCGAGCGGGGCC
CCACGTGCACTACCGCTGGGGCACCCATCCGCCCTGCCGCACCTGTACACCTCGGGCCCC
ACGGGGCTCTCAGCTGCTTCTGCCATCCGTGCCGACGGCGTGTGACTGCCGCCGGGG
CAGAGCGCAGACAGTTGCTGGAGATCAAGGCAGTCCTGCCGGACCGTGGCCATCAAGGG
CGTGCACAGCGTCCGGTACCTCTGCATGGGCCGCCAGGGCAAGATGCAAGGGCTGCTTCACT
ACTCGGAGGAAGACTGTGCTTCGAGGGAGGAGATCCGCCAGATGGCTACAATGTGTACCGA
TCGGAGAAGCACCGCCCTCCGGTCTCCGGTACAGCTGCCAACAGCGGAGCTGTACAAGAA
CAGAGGTTTCTTCACTCTCATTCATGCCCATGCTGCCCATGGTCCCAGAGGAGCTG
AGGACCTCAGGGGCCACTTGAATCTGACATGTTCTTCGCCCTGGAGACCGACAGCATG
GACCCATTGGGCTTGTCAAGGACTGGAGGCCGTGAGGAGTCCAGCTTGTGAAAG**TA**
GAGACATGCCGGCTTCACTGTCGCCAGGGGCTGTGGTACCTGCCAGCTGGGGAGC
TGCTTCTACAAGAACAGTCTGAGTCCACGTTCTGTTAGCTTTAGGAAGAAACATCTAGAA
GTTGTACATATTCAAGAGTTTCCATTGGCAGTGCCAGTTCTGACCATAGACTTGTCTGAT
CATAAACATTGTAAGGCTGTAGCTTGGCCAGCTGCTGCCCTGGGCCCATCTGCTCCCTCGA
GGTGTGCTGGACAAGGCTGCTGACTGCTCATGTTCTGCTGTTGAATACCTCCATCGATGGGAAC
TCACCTCTTGGAAAATTCTTATGTCAGGCTGAATTCAGCTTCTGCTGTTGAATACCTCCATCGATGGGAAC
CCCAGGAGCAGCCAGAAGACAGGCACTGAGTTAATTTCAGGAACAGGGTGTATCCACTCTGT
AAACAGGAGGTAATTTCACTCAACCCCATGTTGGGAATTGTATCTATCTACTTCCAGGG
ACCATTGGCCCTTCCAAATCCCTCCAGGCCAGAACAGTGTAGGAGCAGGCCACAG
GCTTCAGGAGTAGGGGAAGCTGGAGCCCCACTCCAGCCCTGGGACAATTGAGAAATTCCCC
CTGAGGCCAGTTCTGTCATGGATGCTGCTGTGAGAATAACTTGTCTCCGGGTGTACCTGC
TTCCATCTCCAGGCCACAGGCCCTCTGCCCACTCACATGCCCTCCCATGGATTGGGGCT
CCCAGGGCCCCCACCTTATGTCACACTGCACTTCTGTTCAAAATCAGGAAAAGAAAAGAT
TTGAAGACCCCAAGTCTTGTCAATAACTTGTGTGAGCAGCGGGGAAGACCTAGAAC
CTTTCCTCCAGCAGTGGTTTCCAACATGATATTATGAGTAATTATTGTATGTACA
TCTCTTATTCTTACATTATTATGCCCTAAATTATTTATGATGTAGTAAAGTGGAGGTTG
TTTGTATATTAAAATGGAGTTGTTGT

FIGURE 22

MRSGCVVVHVWILAGLWLAVAGRPLAFSDAGPHVHYGWGDPIRLRHLYTSGPHGLSSCFLRI
RADGVVDCARGQSAHSLLIEIKAVALRTVAIKGVHSVRYLCMGADGKMQGLQYSEEDCAFEE
EIRPDGYNVRSEKHLRPPVSLSSAKQRQILYKNRGFLPLSHFLPMLPMVPEEPEDLRGHLESD
MFSSPLETDSMDPFGLVTGLEAVRSPSFEK

Signal peptide:

amino acids 1-22

Casein kinase II phosphorylation site.

amino acids 78-82, 116-120, 190-194, 204-208

N-myristoylation site.

amino acids 15-21, 54-60, 66-72, 201-207

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 48-59

FIGURE 23

CCCAGAAGTTCAAGGGCCCCGGCCTCTGCGCTCTGCCGCCGGACCTCGACCTCCTCA
GAGCAGCCGGCTGCCGCCCCGGAAAGATCGCAGGAGGAGCCACCGCCTCTGCTG
CTGCTGCGTACCTGGTGGTCGCCCTGGCTATCATAAGGCTATGGGTTTCTGCCAAA
AGACCAACAAGTAGTCACAGCAGTAGAGTACCAAGAGGTATTTAGCCTGCAAAACCCAA
AGAAGACTGTTCTCCAGATTAGAGTGGAAAGAAACTGGGTCGGAGTGTCTCCTTGTCTAC
TATCAACAGACTCTCAAGGTGATTTAAAATCGAGCTGAGATGATAGATTCAATATCCG
GATCAAAATGTGACAAGAAGTGTGCGGGAAATCGTTGTGAAGTTAGTGCCTCATCTG
AGCAAGGCCAAAACCTGGAAGAGGATAACAGTCACCTGGAAGTATTAGTGGCTCCAGCAGT
CCATCATGTGAAGTACCCCTTCTGCTCTGAGTGGAACTGTGGTAGAGCTACGATGTCAAGA
CAAAGAAGGAAATCCAGCTCTGAATACACATGGTTAAAGGATGGCATCCGTTGCTAGAAA
ATCCCCAGACTGGCTCCCAAAGCACCAACAGCTACACAACTGAATACAAAAGTGGAACT
CTGCAATTAAATCTGTTCCAAACTGGGAACTGGGAAACGAATGCAAGTAGATGATCTAACATAAGTGGCA
TGTTGGATATCGCAGGTGCTGGGAAACGAATGCAAGTAGATGATCTAACATAAGTGGCA
TCATAGCAGCGTAGTAGTTGTGGCCTTAGTGATTTCCCTTGTGGCCTTGGTGTATGCTAT
GCTCAGAGGAAAGGCTACTTTCAAAAGAACCTCCCTCCAGAAGAGTAATTCTTCATCTAA
AGCCACGACAATGAGTGAAAATGTGCGAGTGGCTCACGCCGTAAATCCAGCATTGGAGG
CCGGCGGGCGGATCACGAGGTCAAGGAGTTCTAGACCAGTCTGGCAATATGGTGGAAACCC
CATCTCTACTAAAATACAAAATAGCTGGCATGGTGGCATGTGCGCTGCAGTTCCAGCTGC
TTGGGAGACAGGAGAATCACTGAACCCGGAGGCGGAGGTTGCACTGAGCTGAGATCACGC
CACTGCAGTCCAGCCTGGGTAACAGAGCAAGATTCCATCTAAAAAATAAAATAATA
AATAAAATCTGGTTTACCTGTAGAATTCTTACAATAATAGCTTGATATTG

FIGURE 24

MARRSRHRLLLLLRLVVALGYHKAYGFSAPKDQQVVTAVEYQEAILACKTPKKTVSSRLE
WKKLGRSVSFVYYQQTLQGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQQQNLEED
TVTLEVLVAPAVPSCEVPSSALSGTVVELRCQDKEGNPAPEYTWFKDGLRLLENPRLGSQST
NSSYTMTKGTQFNTVSKLDTGEYSCEARNNSVGYRRCPGKRMQVDDLNISGIIIAAVVVA
LVISVCGLGVCYAQRKGYFSKETSFQKSNSSSKATTMSENVQWLTPVIPALWKAAGGSRGQEF

Signal peptide:

amino acids 1-20

Transmembrane domain:

amino acids 130-144, 238-258

N-glycosylation site.

amino acids 98-102, 187-191, 236-240, 277-281

Casein kinase II phosphorylation site.

amino acids 39-43, 59-63, 100-104, 149-153, 205-209, 284-288

N-myristoylation site.

amino acids 182-188, 239-245, 255-261, 257-263, 305-311

Amidation site.

amino acids 226-230

09902615-071001

FIGURE 25

GACATCGGAGGTGGGCTAGCACTGAAACTGTTTCAAGACGAGGAAGAGGAGGAGAAAGAG
AAAGAAGGAAAGATGTTGGCACATTAACTTAAACATGCTCCACAGCCGGACCTGGCAT
CATGCTGTATTCCCTGCAAATACTGAAGAAGCATGGGATTAAATATTCTAAATAA
ATGAATTACTCAATCTCTATGACCATCTATACATACTCCACCTTCAAAAAGTACATCAATA
TTATATCATTAAAGGAATAGTAACCTCTTCTTCTCAATCAGCTCTATTGAACCTACTGACTG
CAATTGTCGCACTGCACTTATTCTAGTGAAGAAAACCTTGTGGTTCTATGGCATCATCA
TTTGACAATGCAAGCATCTTCTTATCAATCAGCTCTATTGAACCTACTGACTGACTG
TCCAATTCTATGCTACTTGGCTAGTCACTACACTAGTACAGCTGTAGATAAAAAG
TGGATTGTCCACGGTTATGTACGTGTAAATCAGGCTTGGTTACACCCAGATCCATTAT
ATGGAAGCATCTACAGTGGATTGTAAATGATTAGGTCTTTAACTTCCAGGCCAGATTGCC
AGCTAACACACAGATTCTCTCTACAGACTAACATAATTGCAAAAATTGAATACTCCACAG
ACTTTCAGTAAACCTTACTGGCTCTGGATTATCTCAAAACAAATTATCTTCACTGACCAAT
ATTAATGTAAGGAAAGATGCTCTCAGCTCTTCTGTGTAACCTAGAGGAAACAAACTACTGA
ACTCTGCAACCTTACTGGCTTGTGCAACTGAGCAACTTACAAAGAACCTATATACTACAAC
TGCTTTCTACAAATTTCACCTGGAGCTTATGGGCTACATAATCTTCTCGACTTCATCTC
AATTCAAAATAGATGTCAGATGATCAACAGTAAGTGGTTGATGCTCTCCAAATCTAGAGAT
TCTGATGATTGGGAAAATCCAATTACAGAACTCAAAGACATGAACCTTAAGCCTCTTATCA
ACTTTCGCAACCTGGTTATGCTGATAACCTCACAGAAAATACCAAGATAACGCCCTGGTT
GGACTGAAAATCTAGAAAGCATCTTTCAGATAACAGGCTTATAAAGTACCCCATGT
TGCTCTCAAAAAGTGTAAATCTCAAATTGGATCTAAATAAAAATCCTATTAAATAGAA
TACGAAAGGGTGATTAGCAATATGCTACACTAAAGAGTGGGATAAAATATGCT
GAGCTGATTTCATCGATAGTCTGCTGTGATAACCTGCCAGATTAAAGAAAATAGAAGC
TACTAACACCCTAGATTGCTTACATTACCCCCATGCACTTTCAGACTCCCCAAGCTGG
AATCACTCATGCTGACACGAACTGCTCTCAGTGGCTCTGACCATGGTACCTGACTCTG
CCAAACCTCAAGGAATCAGCATACAGTAACCCCATCAGGTGTGACTGTGTCATCGTTG
GATGAACATGAACAAAACCAATTCTGATTCTGGACAGATTACTGTTTGTGTTGGACC
CACCTGAATTCAAGGTCAAGATGTTGGCAAGTGCAATTTCAGGGACATGATGGAATTG
CTCCCTCTTATAGCTCTGGAGCTTCTCTTCAATCTAAATGAGCTGGGAGCTATGT
TTCTCTTCACTGTAGAGCTACTGCAAGAACACAGCTGAAATCTACTGGATAACACCTTG
GTCAAAACTCTTGCCTAATACCCGACAGACAAGTTCTATGTCATTCTGAGGGAAACACTA
GATATAATGGCGTAACTCCTAAAGAAGGGGTTTATATACTTGATAGCAACTAACCTAGT
TGGCGCTGACTTGAAGTCTGTTATGATCAAAGTGGATCTTCCACAGATAACATG
GCTCTTGAATATTAAGAGATATTAGGCAATTCACTGTTTGTGCTGGAAAGCA
AGTTCTAAATCTCAAATCTAGTGTAAATGGACAGCCTTGTCAAGACTGAAAATTCTCA
TGCTGCGCAAGTGTGCAATACCATCTGATGTCAGGATATCTTACTCATCTGAATC
CATCAACTGAGTATAAAATTGTTATGATATTCCCACCATCTAGAGAAAACAGAAAAAA
TGTGTAATGTCAACCACCAAGGTTGCAACCTGATCAAAAGAGTATGAAAAGATAATAC
CACAAACACTTATGGCCTGCTTGGAGGCCCTCTGGGATTATTGGTGTGATATGCTTATCA
GCTGCCATCTCCAGAAAATGAACACTGTGATGGGACACAGCTATGTGAGGAATTACTACAG
AAACCAACCTTGCAATTAGGTGAGCTTATCTCCTCTGATAATCTCTGGAAAGCAGGAAA
AGAAAAAAAGTACATCACTGAAAGTAAAGCAACTGTTAGGTTACCAACAAATATGTC
AAAAACCCACCAAGGAAACCTACTCCAAAATGAAC

FIGURE 26

MKDMPLRIHVLLGLAITTLVQAVDKVDCPRLCTCEIRPWFTPRTSIYMEASTVDCNDLGLLT
FPARLPANTQILLQTNNAKIEYSTDFFPVNLTLGDLQSNQNLSSVTNINVKKMPQLLSVYLE
ENKLTTELPEKCLSELSNLQELYINHNLLSTISPAGAFICLHNLLRLHNSNRLQMINSKWFDA
LPNLEILMIGENPIIRIKDMNFPLINLRLSIVIAGINILTEIPDNALVGLENLESISFYDNRL
IKVPHVALQKVNNLKFLLDNKNPINRIRRGDFSNMLHLKELGINNMPELISIDSALAVDNLPD
LRKIEATNNPRLSYIHPNAFFRLPKLESLMLNSNALSALYHGTTIESLPNLKEISIHSNPIRC
DCVIRWMNMNKTNIRFMEDPSLFCVDPPEFQGQNVRFQVHFRDMMEICLPLIAPEFSNPNLV
EAGSYVVFHCRATAEPPPEIYWTPSGQQLLPNTLTDKFYVHSEGTLDINGVTPKEGGLYTC
IATNLVGAIDLKSVMIKVDGSPQDNNGSILNIKIRDIDQANSVLVSWKASSKILKSSVKWTAFV
KTENSHAAQSARIPSDVVKVYNLTHLNPSBYKICIDIPITYQKNRKCCVNVTTKGLHPDQKE
YEKNNNTTLMACLGGLGIIVICLISCLSPEMNCDDGHSYVRNYLQKPTFALGELYPPLIN
LWEAGKEKSTSILVKVATVIGLPTNMS

Signal sequence:

amino acids 1-22

Transmembrane domain:

amino acids 633-650

N-glycosylation site.

amino acids 93-97, 103-107, 223-227, 382-386, 522-526, 579-583,
608-612, 624-628, 625-629

Casein kinase II phosphorylation site.

amino acids 51-55, 95-99, 242-246, 468-472, 487-491

Tyrosine kinase phosphorylation site.

amino acids 570-579

N-myristoylation site.

amino acids 13-19, 96-102, 158-164, 221-227, 352-358, 437-443,
491-497, 492-498, 634-640, 702-708

Cell attachment sequence.

amino acids 277-280

FIGURE 27

FIGURE 28

MNLVDLWLTRSLSMCLLQSFVLMILCFHSASMCPKGCLCSSGGLNVTCSNANLKEIPRDL
PPETVLLYLDQNQITSIPNEIFKDLHQQLRVLNLSKNGIEFIDEHAFKGVAETLQTLDSLDR
IQSVHKNAFNNLKRARIANNPWHCDCTLQQVLRSMASNHETAHNVICKTSVLDEHAGRFL
NAANDADLCNLPKKTTDYAMLVTMFGWFTMVISYVVYYVRQNQEDARRHLEYLKSLPSRQKK
ADEPDDISTVV

Signal sequence:

amino acids 1-33

Transmembrane domain:

amino acids 205-220

N-glycosylation site.

amino acids 47-51, 94-98

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 199-203

Casein kinase II phosphorylation site.

amino acids 162-166, 175-179

N-myristoylation site.

amino acids 37-43, 45-51, 110-116

FIGURE 29

FIGURE 30

MQVSKRMLAGGVRSMPSPLLACWQPILLVLGSVLSGSATGCPPRCBCSAQDRAVLCHRKCF
VAVPEGIPTETRLLDGKNRIKTLNQDEFASFPHLEELNENIVSAVEPGAFNNLFNLRTL
GLRSNRKLIPILGVFTGLSNLTKQDISENKIVILLDYMFQDLYNLKSLEVGDNDLVYISHR
FSGLLNSLEQILTLEKCNLTSIPTEALSHLHGLIVLRLRHLNINAIRDYSFKRLYRLKVLEISH
WPYLDTMTPNCLYGLNLTSLSITHCNLTAVPYLAVRHLVYLRFNLNSYNPISTIEGSMMLHEL
LRLQEIQLVGGQLAVVPEYAFRGLNYLRLVNVSGNQLTTLEESVFHSVCNLETLLDSNPLA
CDCRLLNVFRRLWRLNFNRQOPTCATPEFVQGKEFKDFPDVLLPNYFTCRRARIRDRKAQQV
FVDEGHTVQFVCRADGDPPIALWLSPRKHLVSAKNSNGLTVFPDGTLEVRYAQVQDNGTYL
CIAANAGGNDSMPAHLHVRSYSPDWPHQPNKTFAFISNQFGEGEANSTRATVPFPFDIKTLI
IATTMGFISFLGVVLFCLVLLFLWSRGKGNTKHNIEIYVPRKSDAGISSADAPRKFNMKMI

Signal sequence:

amino acids 1-41

Transmembrane domain:

amino acids 556-578

N-glycosylation site.

amino acids 144-148, 202-206, 264-268, 274-278, 293-297, 341-345,
492-496, 505-509, 526-530, 542-546

Casein kinase II phosphorylation site.

amino acids 49-53, 108-112, 146-150, 300-304, 348-352, 349-353,
607-611

Tyrosine kinase phosphorylation site.

amino acids 590-598

N-myristoylation site.

amino acids 10-16, 32-38, 37-43, 113-119, 125-131, 137-143,
262-268, 320-326, 344-350, 359-365, 493-499, 503-509, 605-611

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 32-43

FIGURE 31

CCACCGCGTCCGACCTCGCCCCGGGCTCCGAAGCGCTCGGGGGCGCCCTTCGGTCAAC
ATCGTAGTCACCCCCCTCCCATCCCCAGCCCCGGGATTCAAGGCTGCCAGGCCAGCC
AGGGAGCCGGCGGGAAAGCGCGATGGGGGCCCAGGCCCTCGCTCTGCTCCTGCTCCCTG
TGTTCGCCCTGCTGGCGCCCGCGGGGCAACCTCTCCAGGACGACAGCCAGCCCTG
ACATCTGTGAAACAGTGGTGGCTGGTGCACCGTGGTCTCAAGTGCCAAGTGAAGATCA
CGAGGACTCATCCCTGCAATGGTCAACCTGTCAGCAGACTCTACTTTGGGAGAAGA
GAGCCCTTCGAGATAATCGAATTCACTGGTGTACCTCTACGCCAACGAGCTCAGCATCAGC
ATCAGCAATGTGGCCCTGGCAGACGAGGGCAGTACACCTGCTCAATCTCACTATGCCCTG
GCGAAGCTGCCAAGTCCCTGTCAGTGTCTAGGAATTCCACAGAACGCCATCATCAGTGGT
ATAAAATCTTCATTACGGAAAAAGACACAGCCACCTAACTGTCAGTCTCTGGAGCAAG
CCTGCAGCCGGCTACCTGGAGAAAGGGTACCAAGAACCTCCACGGAGAACCAACCGCAT
ACAGGAAGATCCCAATGGTAAACCTTCAGTGTGACAGCTCGGTGACATTCCAGGTTACCC
GGGAGGATGATGGGGCAGACATCGTGTCTGTGAACCATGAATCTAAAGGGAGCTGAC
AGATCCACCTCTAACGCATTGAAGTTTATAACACACCAACTGCGATGATTAGGCCAGACCC
TCCCCATCTCGTGAGGGCAGAACGCTGTTCTACACTGTGAGGGTGCAGGCAATCAGTC
CCCAGCAGTACCTATGGGAGAAAGGAGGGCAGTGTGCCCCCTGAAGATGACCCAGGAGAGT
GCCCTGATCTCCCTTCCCAACAAGAGTACAGTGGCACCTACGGCTGCACAGCCACCA
CAACATGGCAGCTAACGGCTACTACACCCCTAATGTTAATGCCAGTCCGGTCCCT
CCTCCCTCAGCACCTACACGCATCATGGGGATCGTGGCTTCATTGTCTCTGCTG
CTCATCATGCTCATCTCCCTGGCACTACTTGATCGGACAAAGGAACTACCTGACACA
TGAGGCAAAAGGCTCGACGATGCTCCAGACGCCAACGCCATCATCAATGAGGGC
GGCAGTCAGGAGGGACGACAAGAAGGAATTTCATCAAGGGCGCTGCCACTCCCTG
GCCCCCAAGGGGCCGTGGGACTGCTGGGGCGTCACCAACCCGGACTTGTACAGAGCAA
CCGCAGGGCCGCCCTCCGCTGCTCCAGGCCACCCACCCCTGTACAGAATGTCTGC
TTGGGGTGCCTTGTACTCGGTTGGAAATGGGAGGGAGGGAGGGGGGGAGGGAGGG
TTGCCCTCAGCCCTTCCGTGGCTCTGCATTGGTTATTATTATTTGTAACAAATCC
CAAATCAAATCTGCTCCAGGCTGGAGAGGCAGGAGCCCTGGGTGAGAAAAGCAAAAAACA
AACAAAAAACAA

FIGURE 32

MGAPAASLLLLLFFACCWAPGGANLSQDDSQWPWTSDETVVAGGTVVLCQVKDHEDSSLQW
SNPAQQTLYFGEKRALRDNRIQLVTSTPHELSIISNVALADEGEYTCISIFTMPVRTAKSLV
TVLGIPQKPIITGYKSSLREKDTATLNCQSSGSKPAARLTWRKGDQELHGEPTRIQEDPNGK
TFTVSSSVTFQVTREDDGASIVCSVNHESLKGADRSTSQRIEVLYTPTAMIRPDPPHPREGQ
KLLLHCEGRGNPVPQQYLWEKEGSVPPLKMTQESALIFPFLNKSDSGTYGCTATSNMGSYKA
YYTLNVNDPSPVPSSSSTYHAIIGGIVAFIVFLLLIMLIFLGHYLIRHKGTYLTHEAKGSDD
APDADTAIINAEGGQSGGDDKKEYFI

Signal sequence:

amino acids 1-20

Transmembrane domain:

amino acids 331-352

N-glycosylation site.

amino acids 25-29, 290-294

Casein kinase II phosphorylation site.

amino acids 27-31, 35-39, 89-93, 141-145, 199-203, 388-392

N-myristoylation site.

amino acids 2-8, 23-29, 156-162, 218-224, 295-301, 298-304,
306-310, 334-340, 360-364, 385-389, 386-390

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 7-18

FIGURE 33

GGGGGTTAGGGAGGAAGGAATCCACCCCCCACCCCCCACCACCCCTTCTCTCCCTTCTGG
CTTCGGACATTGGAGCACTAAATGAACCTGAATTGTCTGTGCGAGCAGGATGGTCCTG
TTACTTTGTGATGAGATCGGGATGAATTGCTCGCTTAAATGCTGCTTGGATTCTGTT
GCTGGAGACGCTCTTTGTTGCGCTGAAACGTTACAGGGGAGCTTGCCTGGAAAGAGAAGA
TCTGTTCTGCAATGAGATAGAAGGGGACCTACACGTAAGCTGAAAGAAAAGGGCTTCACA
AGTCTGCAGCGTTTCACTGCCCGACTTCCAGTTTACCATTTTCTGCATGCCAATT
CTCACTCGACTTTCCCTAATGAGTCGCTAACTTTTATAATGCGGTTAGTTGCACATGG
AAAACAATGGCTTGCATGAAATGTCGCCCCGGCTTCTGGGCTGCAAGCTGGTAAAGG
CTGCACATCAACAACAACAGATCAAGTCTGGAAAGCAGACTTTCTGGGCTGGACGA
TCTGGAATATCTCAGGCTGATTAAATTATTACAGAGATATAGACCCGGGGCTTCAGG
ACTTGAAACAAGCTGGAGGTGCTCATTTAAATGACAATCTCATCAGCACCCCTACCTGCCAAC
GTGTTCCAGTATGTCGCCATCACCCACCTCGACCTCCGGGTAACAGGCTGAAAACAGCTGCC
CTATGAGGAGGCTTGGAGCAAACTCTGGTATTGCGGAGATCTGCTAGAGGATAACCCCT
GGGACTGCACCTGTGATCTGCTCCCTGAAAGAATGGCTGGAAACATTCCTCAAAGATGCC
CTGATCGGGCGAGTGTGCTGCAAGGCCCCCAGCAGTCAGGCTAAAGAACCTCAATGAAAC
CCAGGAACAGGACTTGTCTTTGAAAACCGAGTGGATTCTAGTCCTCCGGCGCCCTG
CCCAAGAAGAGACCTTGTCTGGACCCCTGCCACTCTTCAAGACAAATGGGCAAGAG
GATCATGCCACACCAAGGGTCTGCTCAAACGGAGGTACAAAGATCCAGGAACCTGGCAGAT
AAAATCAGGGGCAACAGCAGCGATAGCGAGGGTAGCTCCAGGAACAAACCCCTAGCTAACA
GTTTACCCCTGCCCTGGGGCTGAGCTGCGACCATCCTCAGGGTCTGGTTAAAGATGAAC
TGCAACAACAGGAACGTGAGCAGCTGGCTGATTGAAGGCCAACGCTCTAACGTGCAAGGA
GCTTTTCTACAGATAACAGATCCACAGCTCCGAAATCGCACTTGTGGATTACAAGA
ACCTCATCTGTGTTGGATCTGGCAACATAACATCCTACTGTAGAGAACAAACACTTCAAG
AACCTTTGGACCTCAGGGCTTACATGGATAGCAATTACCTGGACACGCTGTCCTGGGA
GAAATCTGGGGCTGCAAACACTAGAGTACCTGAACTGGAGTACAACGCTATCCAGCTCA
TCCTCCGGGACTTCAATGCCATGCCAAACTGAGGATCTCATTCTCAACAAACACTG
CTGAGGCTCTGCTGTGGAGCTGTCCTGGGGTCTGCTCTCTAACATCAGCTGCAACAA
CAATTACTCATGTACCTCCGGTGGCAGGGTGTGGACCAGTTAACCTCCATCATCCAGA
TAGACCTCCACGGAAACCCCTGGAGTGTCTGCACAAATTGTGCTTCTAACGAGTGGCA
GAACGCTTGGGTTCCGAAGTGTGATGAGGCCACCTCAAGTGTGAGACGCCGGTGAACCTCT
TAGAAAGGATTTCATGTCCTCTCCAAATGAGCAGAGATCTGCCCTCAGCTGTACGCTAGGATCT
GCCAACGCTTAACCTGGCACAAGTAAAACAGCAGTCAGGTTGGGGAGACGGGAGCAGCTCC
AACTCTTACCTAGACACCCAGGGCTGTCATCTGGTCTGGGTCCCCGACTGCTGCTGGT
GTTGTCACCTCCGGCTTCACCGTGGTGGCATGCTGTGTTTATCTGAGGAACCGAAAGC
GGTCCAAGAGACGAGATGCCAACTCCTCCGCTCGAGGATTAATTCTACAGACAGTCTG
GACTCTCTTACCTGGCACAATGGCCTTAACACGAGATGGGGCCACAGAGTGTATGACTG
TGGCTCTACTCGCTCTAGACTAAAGACCCCAACCCCATAGGGAGGGCAGAGGGAGGG
ATACATCTTCCCAACCGCAGGCACCCGGGGCTGGAGGGGCTGTACCCAAATCCCCGG
CCATCAGCCTGGATGGGATAAGTAGATAATAACTGTGAGCTGCCACAACCGAAAGGGCT
GACCCCTTACTTAGCTCCCTCTTGAAAACAGAGCAGACTGTGGAGAGCTGGAGAGCGCA
GCCAGCTGCTCTTGTGAGAGCCCCCTTGTGACAAAGGCCAGCACGCCCTGCTGGAG
AACTGACAGTGCCTCGCCCTGGCCCCGGGGCTGTGGGGTTGGATGCCGGTTCTATAC
ATATATACATATATCCACATCTATAGAGAGATAGATATCTATTCTCCCTGTGGATTAG
CCCCGTGATGGCTCCCTGTGCTACGCAAGGATGGGCAAGTGTGACAGGCAAGGATGAATGTAT
TGAAAAGTAAGTAACCTTGACTTCTGAC

FIGURE 34

MLWILLLLETSLCFAAGNTGVDCKEKICSCNEIEGDLHVDCEKKGFTSLQRFTAPTSQFYH
LFLHGNSLTLRFPEMFANVSHMENNGHLH1VPGALFLQLQVLRHLH1NNNKIKSFRKQ
TFLGLDDLLQADFNLRLDIPGAQDQDLNKLLEVLI1NDNLISTLPANVQYVPIHTLDRG
NRKLTKLTYEEVLEQ1PGIAEILLENPDWTCDLNLKWELENIPKNA1LGRVVCAPTRLQ
GKDLNNETTEQDLCPLKNRVDSSLAPPQAETFAPGPPLPTPFKTNGQEDHATPGSAPNGGTK
1PGNNWQ1KIRPTAAIATGSSRNKPLANS1LPCPGGCSCH1IPGSLKMNCCNRRNVSSLADLKP
KLSNVQELFLRDNKIH1TRKSHFVDYKNL1LLDGLNNIAT1VENNTFKNLLDLRVLYMDNSY
DLTSLRSERFKAGLQNLVEYNALQ1LIPGFTNAMPKRL1L1LNNNLLRSLPVDVGFASVSL
SKLSLHNHYFMYLFLPVAGVLDQLTSIIQ1DLHGNPWECSCT1VFPFKQWAERLGSEVIMSDLKC
ETPVNNFRKKDFMLNSDE1CPLYARISPTLTSHSKNSTGLAFTGTHNSYLDTSRVS1S1VL
VGPLL1VFTVSAFTVUGMLVFLRNRKRSKRRDANS SASE1NSLQTVCDSSYWHNGPYNADG
AHRVYDCHGHSLLSD

Signal sequence:

amino acids 1-15

Transmembrane domain:

amino acids 618-638

N-glycosylation site.

amino acids 18-22, 253-257, 363-367, 416-420, 595-599, 655-659

cAMP- and cGMP-dependent protein kinase phosphorylation site-

amino acids 122-126: 646-650

Casein kinase II phosphorylation site.

amino acids 30-34, 180-184, 222-226, 256-260, 366-370, 573-577

608-612 657-661 666-670 693-697

N-myristoylation site

amino acids 17-23, 67-73, 100-106, 302-308, 328-334, 343-349, 354-360, 465-471, 483-489, 598-604, 603-609

Prokaryotic membrane lipoprotein lipid attachment site

amino acids 337-348

FIGURE 35

AGTCGACTGCGTCCCCGTACCGCGCCAGCTGTCTGACCCAGAATAACTCAGGGC
TGCACCGGGCCTGGCAGCGCTCGCACACATTCTGTGCGGCCATAAGGAAACTGTTGGC
CGCTGGGCCCCGGGGGGATTCTTGGCAGTTGGGGGTCGTCGGAGCAGGGCGAGGGG
AAGGGAGGGGAACCGGGTGGGAAGCAGCTGTAGAGGGCGGTGACCGCGCTCCAGACAC
AGCTCTGCGTCTCGAGCGGAGAGATCAAGTTGGCAGCAGCTCTGCCGCGAGGGGGCTCAG
AGAATGAGGCCGGGTTGCCCTGTGCCCTCTCTGGCAGCGCTCTGCCCGGGCGGCG
CGCGAACACCCCACTGCCGACCGTGTGGCTGCTGCCCTCGGGGCGTACAGCCTGC
ACCACGCTACATGAAGCGCAGGGCGCAGGGAGGCTGACCTCTGCCGAGGGTGGGGCGCTC
AGCACCGTGTGCGGGCGGAGCTGCCGCTGTGCTCGCGCTCTGCCGAGGGCCAGG
GCCCGGAGGGGGTCCAAAGACCTGTGTCTGGGTGCCACTGGAGCGCAGGGCTTCCACT
GCACCCCTGGAGAACGAGCTTGTGGGGTTCTCTGTGCTCTGCCGACCCGGCGGTCTC
GAAAGCGACACGCTGAGTGGGGAGGGGGACACGCTCTGCCGACCGCGAGATGCGC
GGTACTCCAGGCCACCGGGGGTGTGAGCTGGGGAGGGAGATGCGATGCCACCTGC
GCCCAACGGCTACCTGTGCAAGTACCAAGTTGAGGTCTGTGCTCTGCCGCGCCCCGGG
GCCGCTCTAACCTGAGCTGGGGCCCTTCACTGCAAGCTGGGGAGGCTCTGGAGCTTCA
TCCACCTGGGACGGAGGGTGAAGTGCCTCTGCCGGGAGACAGCTCGGATCTCA
TCGCGACGAAATCGCGCTCGCTGGACAAACTCTGGGGCGATGTTGTCTCTGCC
GGGAGGTACCTCCGTGTCGCAAATGCGAGCTCCCTAAGCTGCTAGACGACTTGGAGG
CTTGCCCTGCAATGTGCTACGGGCTTGGAGCTGGGGAGGGACGGCCGCTCTGTGACCA
GTGGGGAAAGGACAGCCGACCCCTGGGGGAGGGTGGCCACAGGGCGCCCGGCCACT
GCAACAGCCCGTGGCGAGAAACATGCCAATCAGGTGCGACAGAGAAGCTGGAGAGAC
ACCACCTGTCTCTAACACAAGACAATTCACTGAAACATCTTCTGAGATTCTCGATGGGAT
CACAGAGCAGCATGTCACCTTCAAATGCTCCCTCAAGCCGAGTCAAAGGCCACTATCACC
CCATCAGGGAGCGTGATTCCAAGTTAACTACAGCTTCTGCCACTCCTCAGGCTT
GCACTCTCTCTGCCGTGGCTTCATATTGTGAGCACAGCAGTAGTAGTGTGGTGTACT
TGACCATGACAGTACTGGGCTTGTCAAGCTCTGCTTCACGAAAGGCCCTCTCCAGCCA
AGGAAGGAGTCTATGGGCCCGGGCTGGAGAGTGTACCTGAGGCCGCTGCTTGGCTC
CAGTTCTGCACATTGCACAAACAATGGGGTGAAGTGGGGACTGTGATCTGCCGACAGAG
CAGAGGGTGCCTTGTGGGGAGTCCCCCTTGGCTACTGTGATGCACTAGGAAACAGGGGA
CATGGGCACTCTGTGAAAGTTTCACTTTGATGAAACAGGGGACCAAGAGGAACCTTAC
TTGTGTAAGTGACAATTCTGCAGAAATCCCCCTCTCTAAATTCCCTTACTCCTGAG
GAGCTAAATCAGAAACTGCAACTCTTCTCTGATGATAGAGGAAGTGAAGTGCCTTACGAG
TGGTGTACTGGGGACGGGTAGTGTGGGGAGAGATATTCTTATGTTTATTCCGGAGAA
TTTGGAGAAGTGTGAACCTTCTAACAAAATGAAAGGAAATGTTCTATGTTCTCAGGCTAGGAGTAT
TTAAAAATAATTCTACCAAAATGAAAGGAAATGTTCTATGTTCTCAGGCTAGGAGTAT
ATTGGTCGAAATCCCAGGGAAAAAATAAAAAATAAAAAATAAAGGATTGTTGAT

FIGURE 36

MRPAFALCLLWQALWPAGPGGGEHPTADRAGCSASGACYSLHHATMKRQAAEEACILRGGALS
TVRAGAELRAVLALLRAGPGPGGSKDLLFWVALERRSHCTLENEPLRGFSWLSSDPGGL
SDTLLQWVEEPQRSCTARRCAVLQATGGVEPAGWKEMRCHLRANGYLCKYQFEVLCPAPRPG
ASNLSSYRAPFQLHSAALDFSPPGTEVSALCRGQLPISVTCIADEIGARWDKLSGDVLCPCPG
RYLRAGKCAELPNCLDDILGGFACECATGFELGKDGRSCVTSGEGQPTLGGTGVPTRPPATA
TSPVPQRTWPIRDEKLGETPLVPEQDNSVTSIPEIPRWGSQSTMSTLQMSLQAESKATITP
SGSVISKFNSTTSSATPQAFDSSSAVVFIFVSTAVVVLVILMTVLGLVKLCFHESPSSQPR
KESMGPPGLESDEPEPAALGSSSAHCTNNGVKVGDCDLRDRAEGLLAESPLGSSDA

Signal sequence:

amino acids 1-16

Transmembrane domain:

amino acids 399-418

N-glycosylation site.

amino acids 189-193, 381-385

Glycosaminoglycan attachment site.

amino acids 289-293

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 98-102, 434-438

Casein kinase II phosphorylation site.

amino acids 275-279, 288-292, 342-346, 445-449

N-myristoylation site.

amino acids 30-36, 35-41, 58-64, 59-65, 121-127, 151-157,
185-191, 209-215, 267-273, 350-356, 374-380, 453-459, 463-469,
477-483

Aspartic acid and asparagine hydroxylation site.

amino acids 262-274

009002615 - 0711001

FIGURE 37

CGGACGCGTGGGATTCAACAGTGGCCTGTGGCTGCCAGAGCAGCTCCCTCAGGGGAAACTAAG
CGTCGAGTCAGACGGCACCATAAATCGCCTTAAAGTGCCTCCGCCCTGCCGCCGCGTAC
CCCCGGCTACCTGGGCCGCCCGCGCGGTGCGCGCTGAGAGGGAGCGCGCGGCCAGCGGA
GCGCGCTGTGAGCCAGCGCTGCGCAAGTGTGAGCGCGGTGAGCGCGCTGGGTGCGGA
GGGGCGCTGTGCCCCCGCGCCCGCTGGGTGCAAAACCCGAGCGTCTACGCGTGCCTAATGA
GGGGCGCGAACCGCTGGGCCCACTCTGCGTGTGGCTGCCACCCAGCTCTCGGG
CAGCAGTCCCCAGAGAGACCTGTTTACATGTGGTGGCATCTTACTGGAGAGTCGGATT
TATTGGCAGTGAAGGTTTCTGGAGTGTACCCCTCAAAATGCAATGGAAAATCA
CAGTTCCGAAGGAAAATGAGTAGTCGTTCTAATTCGATTATGACACTCGAGAGTGACAAC
CTGTGCCGCTATGACTTTGTGGATGTGACAATGGCCATGCCAATGGCCAGCGCATTGGCCG
CTTCTGTGGCACTTCCGGCTGGAGCCCTGTGTCAGTGGCAACAAAGATGATGGTGCAGA
TGATTTCGTATGCCAACACAGCTGGCAATGGCTCATGGCCATGTTCTCGCTGCTGAAACCA
AACAAAGAGGGGATCACTATTGTGGAGGACTCCTGACAGACCTTCGGCTCTTTAAAC
CCCCAACTGGGAGACCGGGATTACCCCTGCGAGGAGTCATTTGTGTGGCACATTGTAGCCC
CAAAGAATCAGCTTATAGAATTAAAGTGTGAGAATTGTGATGTGGAGGAGATAACTACTGC
CGATATGATTATGTGGCTGTGTTAATGGCGGGAACTCAACGATGCTAGAAGAAATTGGAAA
GTATTGTGGTGTAGTCACCTCGGCCAATTGTGCTGTGAGAAGAAATGAACCTTCTTATTCACT
TTTATCATGAGCTTAAGTTAACTGAGATGGGTTTATGGTCACTACATATTCAAGGCCAAA
AAACTGCTCAACTACAGAACAGCGCTGCAACACCACATTCTGTAAACCACGGGTTAAA
ACCCACCGTGGCTTGTGTCACAAAAGTGTAGACGGACGGGACTCTGGAGGGCAATTATT
GTTCAAGTGACTTGTATTAGCCGGACTGTTATCACAAACCATCACTCGCGATGGGAGTTG
CACCCCAAGCTCGATCATCAACATCTACAAAGAGGGAAAATTGGCATTAGCGAGCGGG
CAAGAACATGAGTGGCAGGCTGACTGCTGCTGCAAGCAGTGCCTCTCTCAGAAGAGGT
TAAATTACATTATTGGGCAAGTAGGTGAAGATGGGAGGCAAATCATGCCAAACAGC
TTTATCATGATGTTCAAGACCAAGAATCAGAAGCTCTGGATGCCCTTAAAATAAGCAATG
TAAAGTGACTGTGTCATTAAAGCTGATTCTGCAATTGCCCATTGCTTAAAGAGATCTATGTT
TCTCAGTAGAAAAAAATACTTATAAAATTACATATTCTGCAAAGAGGATTCCGAAGAGATGG
GACTGGTTGACTCTTCACATGATGGAGGTATGAGGCCCTCGAGATAGCTGAGGGAAAGTTCT
TGCCTGCTGTGAGAGGAGCAGCTATCTGATTGGAAACCTGCCACTTAGTGCAGGTGATAGGA
AGCTAAAAGTGTCAAGCGTTGACAGCTTGAAGCGTTATTTATACATCTGTAAAAGGAT
ATTTAGAATTGAGTTGTGTAAGATGTCAAAAAAAAGATTTAGAAGTGCACATTATAGT
GTTATTGTGTTACCTTCAAGCCTTGGCCCTGAGGTGTTACAATCTTGTCTTGCCTTCTA
AACTCAATGCTTAAATAAAATTTTAAAGGAAAAAA

FIGURE 38

MRGANAWAPLCLLLAATQLSRQQSPERPVFTCGGILTGESGFIGSEGFPGVPPNSKCTWK
ITVPEGKVVLNFRFIDLESNDLCRYDFDVYNGHANGQRIGRFCGTFRPGALVSSGNKMMV
QMISDANTAGNGFMAMFSAAEPENRGQDQYCGGLLDRPSGSFKTPNPDRDYPAVGTCVWHIV
APKNQLIELKFKEFDVERDNYCRYDYVAVFNGGEVNDARRIGKYCGDSPAPIVSERNELLI
QFLSDLSLTADGFIGHYIFRPKKLPTTTEQPVTTTFPVTTGLKPVALCQQKCRRTGTLEGN
YCSSDFVLAGTVITITRDGSLHATVSIINIYKEGNLAIQQAGKNSARLTVVCKQCPPLLRR
GLNYIIMQVGEDGRGKIMPNSFIMMFKTKNOKLLDALKNKC

Signal sequence:

amino acids 1-23

N-glycosylation site.

amino acids 355-359

Casein kinase II phosphorylation site.

amino acids 64-68, 142-146, 274-278

Tyrosine kinase phosphorylation site.

amino acids 199-208

N-myristoylation site.

amino acids 34-40, 35-41, 100-106, 113-119, 218-224, 289-295, 305-311, 309-315, 320-326, 330-336

Cell attachment sequence.

amino acids 149-152

FIGURE 39

CGGACGCGTGGCGGACCGGTGGGCGGCCACGGCGCCCGGGCTGGGCGGTGCTTCTT
CTTCTCCGTGGCCTACGAGGGTCCCCAGCCTGGTAAAGATGGCCCCATGGCCCCGAAGG
GCCTAGTCCCAGCTGTGCTCTGGGCCTCAGCCTCTCTCAACCTCCCAGGACCTATCTGG
CTCCAGCCCTCTCCACCTCCCCAGTCTCTCCCCGCTCAGCCCCATCCGTGTACACCTG
CCGGGGACTGGTTGACAGCTTAACAAGGGCCTGGAGAGAACCATCCGGACAACTTTGGAG
GTGGAAACACTGCCTGGGAGGAAGAGAATTGTCAAATACAAAGACAGTGTGAGACCCGCTG
GTAGAGGTGCTGGAGGGTGTGCAAGTCAGACTTCGAGTGCACCCGCTGCTGGAGCT
GAGTGAGGAGCTGGTGGAGAGCTGGTGGTTCAAAAGCAGCAGGAGGGCCGGACCTCTTC
AGTGGCTGTGCTCAGATTCCCTGAAGCTCTGCTGCCCGCAGGCACCTTCGGGCCCTCTGC
CTTCCCTGTCTGGGGAAACAGAGAGGCCCTGCGGTGGCTACGGGAGTGTGAAGGAGAAGG
GACAGGAGGGGAGCCGGACTGTGACTGCCAAGCCGCTACGGGGGTGAGGCCCTGCGCC
AGTGTGGCCTGGCTACTTGAAGGCAACGCAACGCCAGCATCTGGTATGTTGCTGGCTTGT
TTGGGCCCTGTGCCGATGCTCAGGACCTGAGGAATCAAACGTGTTGCAATGCAAGAAGGG
CTGGGCCCTGCATCACCTCAAGTGTGTAGACATTGATGAGTGTGGCACAGAGGGAGCCA
ACTGTGGAGCTGACCAATTCTGCGTGAACACTGAGGGCTCTATGAGTGCAGACTGTGCCAAG
GCCTGCCTAGGCTGCATGGGGCAGGCCAGGTGCTGTAAGAAGTGTAGCCCTGGCTATCA
GCAGGGCTTCAAGTGTCTCGATGTGGATGAGTGTGAGACAGAGGTGTGTCGGAGAGA
ACAAGCAGTGTAAAACACCAGGGCGTTATCGCTGCATCTGTGCCAGGGCTACAAGCAG
ATGGAAAGGCATCTGTGTGAAGGAGCAGATCCCAGAGTCAGCAGGCCCTTCTCAGAGATGAC
AGAAGACGAGTTGGTGGTGTGCAAGCAGATGTTGGCATCATCTGTGCACTGGCA
CCCTGGCTGCTAAGGGCGACTTGGTGTGACGCCATCTCATTGGGCTGTGGGCCATG
ACTGGCTACTGGTGTGCAAGCGCAGTGACCGTGTGCTGGAGGGCTTCATCAAGGGAGATA
ATCGCGGCCACCCACTGTAGGACCTCTCCACCCACGCTGCCCGAGCTGGCTGCC
TCCCTGCTGGACACTCAGGACAGCTGGTTATTTTGAGAGTGGGTAAGCACCCTACCTG
CCTTACAGAGCAGCCAGGTACCCAGGCCGGCAGACAAGGCCCTGGGTAAAAGTAGC
CCTGAAGGTGAGATACCATGAGCTCTCACCTGGGGACTGGCAGGCTCACAATGTGTGA
ATTTCAAAAGTTTCTTAATGGTGGTGTAGAGCTTGGCCCTGCTTAGGATTAGGT
GTCCTCACAGGGTGGGGCATCACAGCTCCCTCTGCCAGCTGCATGCTGCCAGTCTGT
TCTGTGTTCACACATCCCCACACCCATTGCCACTTATTATTCATCTCAGGAAATAAAGA
AAGGTCTTGGAAAGTTAAAAAAAAAAAAAAAAAAAAAA

FIGURE 40

MAPWPKKGLVPAVLWGLSLFLNLPGPIWLQPSPPPQSSPPPQPHPCHTCRGLVDSFNKGLER
TIRDNFGGNTAWEENLSKYKDSETRLVEVLEGVVCSKSDFECHRLLELSEELVESWWFHKQ
QEAPDQLFQWLCSDSLKLCCPAGTFGPSCLPGPGTERPCGGYGGQCEGECTRGGSGHCDCQAG
YGGEACGQCGLYFEAERNASHLVCSACFGPCARCSGPEESNCLQCKKGWALHHLKCVDIDE
CTTEGANCAGADQFCVNTEGSYECRDCAKACLGCMGAGPGRCKKCSPGYQQVGSKCLDVDECE
TEVCPGENKCENTEGGYRCICAEGYKQMEGICVKEQIPESEGFFSEMTEDELVVLQQMFFG
IIICALATLAAKGDLVFTAIFIGAVAAMTGYWLSERSDRVLEGFIKGR

Signal sequence:

amino acids 1-29

Transmembrane domain:

amino acids 372-395

N-glycosylation site.

amino acids 79-83, 205-209

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 290-294

Casein kinase II phosphorylation site.

amino acids 63-67, 73-77, 99-103, 101-105, 222-226, 359-363

N-myristoylation site.

amino acids 8-14, 51-57, 59-65, 69-75, 70-76, 167-173, 173-179,
177-183, 188-194, 250-256, 253-259, 267-273, 280-286, 283-289,
326-332, 372-378, 395-401

Aspartic acid and asparagine hydroxylation site.

amino acids 321-333

EGF-like domain cysteine pattern signature.

amino acids 181-193

09902515-071001

FIGURE 41

TGAGACCCCTCTGCAGCCTCTCAAGGGACAGCCCCACTCTGCCTCTGCTCCTCCAGGGCA
GCACCATGCAGCCCCCTGTGGCTCTGCTGGGACTCTGGGTGTTGCCCTGGCCAGCCCCGGG
GCCGCCCTGACCGGGGAGCAGCTCTGGCAGCCTGCTGCCAGCTGAGCTCAAAGAGGT
GCCCACCTGGACAGGGCCACATGGAGGAGCTGGTCACTCCCACCCACGTGAGGGCCAGT
ACGTGGCCCTGCTGCAGCGCAGCCACGGGACCGCTCCCGCGAAAGAGGTTGACCCAGAGC
TTCCGAGGGTGGCCGGCAGGTTCTGGCGTGGAGGGCAGCACACACCTGCTGGTGTTCGG
CATGGAGCAGCGGCTGCCGCCAACAGCGAGCTGGTGCAAGGCCGTGCTGCCGTCTCCAGG
AGCCGGTCCCCAAGGCCGCGCTGCACAGGCACGGCGCTGTCCCCCGCGAGGCCCGGGC
CGGGTGAACCGTCAGTGGCTGCGCGTCCCGACGACGGCTCAACCGCACCTCCCTCATCGA
CTCCAGGCTGGTGTCCGTCACAGAGCGGCTGGAAGGCCCTGACGTGACCGAGGCCGTGA
ACTTCTGCCAGCAGCTGAGGCCGCCCGCAGCCGCTGCTGCTACAGGTGTCGGTGCAGAGG
GAGCATCTGGCCCGCTGGCGTCCGGCGCCACAAGCTGGTCCGTTGCCTCGCAGGGGGC
GCCAGCCGGCTGGGAGCCCAGCTGGAGCTGCACACCCCTGGACCTGGGGACTATGGAG
CTCAGGGCAGCTGTGACCCCTGAAGCACCAATGACCGAGGGCACCCGCTGCTGCCGCCAGG
ATGTACATTGACCTGCAGGGATGAAGTGGCCGAGAACCTGGTGCTGGAGCCCCGGGCTT
CCTGGCTTATGAGTGTGTTGGCACCTGCCCGCAGCCCCCGGAGGCCCTGGCCTCAAGTGGC
CGTTTCTGGGCCTGACAGTCATGCCCTGGAGACTGACTCGCTGCCCATGATCGTCAGC
ATCAAGGAGGGAGGCAGGACCAGGCCAGGTGGTCAGCCTGCCAACATGAGGGTGCAGAA
GTGCAGCTGCGCTCGGATGGTGCCTCGCAAGGAGGCTCCAGCCATAGGCGCCTAGTG
TAGCCATCGAGGGACTTGAATTGTGTTCTGAAGTGTGCTGAGGGTACCGAGAGCTG
GGCATGACTGAACCTGCTGATGGACAAATGCTCTGCTCTAGTGAAGCCCTGAATTGCTT
CCTCTGACAAGTTACCTCACCTAATTGGCTTCTCAGGAATGAGAACATTGGCCACTGG
GAGCCCTGCTCAGTTCTCTATTCTTATTCACTGCACTATATTCTAACGACTTACAT
GTGGAGATACTGTAACCTGAGGGCAGAAAGCCCANTGTCATTGTTACTTGTCTGTAC
TGGATCTGGGCTAAAGCTCCACCAACTCTGGACCTAACGACCTGGGTTAAGTGTGGGT
TGTGCATCCCCAATCCAGATAATAAGACTTGTAAAACATGAATAAACACATTATTCT
AAAA

FIGURE 42

MQPLWLWCALWVLPLASPGAAALTGEQLLGSSLRQLQLKEVPTLDRADMEELVIPTHVRAQYV
ALLQRSHGDRSRGKRFQSFRREVAGRFLALEASTHLLVFGMEQRLPPNSELVQAVLRLFQEP
VPKAALHRHGRGLSPRSARARVTVEWLRVRDDGSNRTSLIDSRLVSVHESGWKAFDVTEAVNF
WQQLSRPRQPLLQVSQVREHGLGPLASGAHKLVRFASQGAPAGLGEPEQLELHTLDLGDYGAQ
GDCDPEAPMTEGTRCCRQEMYIDLQGMKWAENWVLEPPGFLAYECVGTCRQPPEALAFKWPF
LGPRQCIASETDSLPMIVSIKEGGRTRPQVVSLPNMRVQKCSCASDGALVPRLQF

Signal sequence:

amino acids 1-18

N-glycosylation site.

amino acids 158-162

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 76-80

Casein kinase II phosphorylation site.

amino acids 68-72, 81-85, 161-165, 169-173, 319-323, 329-333

N-myristylation site.

amino acids 19-25, 156-162, 225-231, 260-266, 274-280

Amidation site.

amino acids 74-78

TGF-beta family signature.

amino acids 282-298

FIGURE 43

GTCTGTTCCCAGGAGTCCTCGGCGCTGTTGTGTCAGTGGCCTGATCGCGATGGGACAAA
GGCGCAAGTCGAGAGGAAACTGTTGCCCTTCATATTGGCAGTCCTGTCCTGG
CATTGGGCAGTGTACAGTGCACCTTCGAACCTGAAGTCAGAATTCTGAGAAATAATCCT
GTGAAGTTGTCCTGTGCCACTCGGGCTTTCTTCTCCCCGTGTGGAGTGGAAAGTTGACCA
AGGAGACACCAACCAGACTCGTTGCTATAAAACAAGATCACAGCTTCTATGAGGACCGGG
TGACCTTCTGCCAACCTGGTATCACCTCAAGTCCGTGACACGGGAAGACACTGGGACATAC
ACTTGTATGGTCTCTGAGGAAGGCGAACAGCTATGGGAGGTCAAGGTCAAGCTCATCGT
GCTTGTGCCCTCATCCAAGCTACAGTTACATCCCCTCTGCCACCATGGGAAACCGGG
CAGTGCAGATGCTCAGAACAAAGATGGTCCCCACCTCTGAATAACACCTGGTCAAAAGAT
GGGATAGTGTGCTCACGAATCCAAAAGCACCGTGCCTCGACAACTCTCTATGTCT
GAATCCCACAAACAGGAGAGCTGGCTTGTACCTCTGTCAGCTCTGATACTGGAGAATACA
GCTGTGAGGCACGGAATGGGTATGGACACCCATGACTTCAAATGCTGTGCGCATGGAAAGCT
GTGGAGCGGAATGTGGGGTACCTGTGGCAGCGCTCTGTAACCTGATTCTCTGGGAAT
CTTGGTTTTGGCATCTGGTTGCTATAGCCGAGGCCACTTGACAGAACAAAGAAGGGA
CTTCGAGTAAGAAGGTGATTACAGCCAGCCTAGTGGCCGAAGTGAAGGAGAATTCAACAG
ACCTCGTCATTCTGGTGTAGCCTGGTCGGCTCACCGCTATCATCTGATTGCTTACT
CAGGTGCTACCGACTCTGGCCCTGATGTCGTAGTTCACAGGATGCCATTGTCTTC
TACACCCCACAGGGCCCCACTTCTCGGATGTGTTTAATAATGTCAGCTATGTCCCC
ATCCTCTTCATGCCCTCCCTCCCTTCTACACTGCTGAGTGGCTGGAACTTGTAAA
GTGTTTATTCCCCATTCTTGAGGGATCAGGAAGGAATCTGGGTATGCCATTGACTTCCC
TTCTAAGTAGACAGCAAAATGGCGGGGGTGCAGGAATCTGCACTCAACTGCCACTGGC
TGGCAGGGATCTTGAAATAGTGTCTTGAGCTGGTTCTGGCTCTTCTTGACTGAC
GACCAGGGCCAGCTGTTCTAGAGCGGGAAATTAGAGGCTAGAGCGGCTGAAATGGTTTGG
TGATGACACTGGGTCTTCATCTCTGGGCCACTCTCTGTCTTCCATGGGAAGTG
CCACTGGGATCCCTCTGCCCTGCTCTCGAATACAAGCTGACTGACATTGACTGTCTGT
GGAAAATGGGAGCTCTGTGAGAGCATAGTAAAATTTCAGAGAACCTGAAGCCAAAAG
GATTTAAAACCGCTGCTAAAGAAAAGAAAAGTGGAGGCTGGCGCAGTGGCTCACGCCCTG
TAATCCCAGAGGCTGAGGCAGGCGGATCACCTGAGGTGGGAGTTGGGATCAGCTGACCA
ACATGGAGAACCCACTGGAAATACAAGTTAGCCAGGCTGGTGGCATGCCCTGAGTC
CCAGCTGCTCAGGAGCCTGGCAACAAGAGCAAAACTCCAGCTCAAAAAAAAAAAAAAA

FIGURE 44

MGTKAQVERKLLCLFLAILLCSLALGTSVHSSEPEVRIPENNPVKLSCAYSGFSSPRVEWKFDQGDTTRLVCYNNKITASYEDRVTFLPTGITFKSVTREDTGTYTCMVSEEGGNNSYGEVKVKLIVLVPPSKPTVNIPESSATIGNRAVLTCSEQDGSPPESEYTWFKDGVMPNPKSTRAFSNSSYVLPNTTGEVLFDPASDTEGEYSCEARNGYGTPMTSNAVRMEAVERNVGIVIAAVLVTLLIGLILVFGIWFAYSRGHFDRTKKGTSKKVIIYOPSARSERGEFKOTSSFLV

Signal sequence:

amino acids 1-27

Transmembrane domain:

amino acids 238-255

N-glycosylation site.

amino acids 185-189

cAMP- and cGMP-dependent protein kinase phosphorylation site

amino acids 270-274

Casein kinase II phosphorylation site

amino acids 34-38, 82-86, 100-104, 118-122, 152-156, 154-158, 193-197, 203-207, 287-291

N-myristoylation site

amino acids 195-111, 116-132, 158-164, 218-225, 237-243, 256-262

FIGURE 45

CAGCGCGTGGCCGGCGCCGTGTGGGACAGC**A**TGAGCGCGGTGGATGGCGCAGGTTGGA
GCGTGGCGAACAGGGGCTCTGGCCTGGCGCTGCTGCTGCTCGCTCGGCTCGGACTAGGCCT
GGAGGCGCCCGAGCCCGTTCCACCCGACCTCTGCCAGGCCAGGCCCCAGCTCAG
GCTCGTCCCACCCACCAAGTCCAGTGCAGCACCAGTGGCTTATGCGTGCCTCAGCTGG
CGCTGCAGAGGACTTGGACTGCAGCGATGGCAGCGATGAGGAGGAGTGCAGGATTGAGCC
ATGTACCCAGAAAGGGCAATGCCACCGCCCCCTGGCTCCCTGCCCTGCACCGCGTCA
GTGACTGCTCTGGGGAACTGACAAGAAACTGCGCAACTGCAGGCCCTGGCTGCCTAGCA
GGCGAGCTCCGTTGCACGCTGAGCGATGACTGCATTCCACTCACGTGGCGCTGCGACGGCCA
CCCAGACTGTCCCGACTCCAGCAGCGAGCTCGGCTGTGGAACCAATGAGATCCTCCCGAAG
GGGATGCCAACCATGGGCCCCCTGTGACCCCTGGAGAGTGTCACTCTCTCAGGAATGCC
ACAACCATGGGCCCCCTGTGACCCCTGGAGAGTGTCCCTCTGCGGAATGCCACATCTC
CTCTGCCGGAGACCAGTCTGGAAAGCCAATGCCCTATGGGTTATTGCGAGCTGCTGCCGTGC
TCAGTGCAAGGCTGGTCACGCCACCCCTCCCTTTGTCCCTGGCTCCGAGGCCAGGAGC
CTCCGCCACTGGGTTACTGGTGGCCATGAAGGAGTCCCTGCTGTCAGAACAGAAC
CTCGCTGCC**T**GAGGACAAGCAGTGGCACCCGTCACTCAGGCCCTGGCGTAGCCGGACA
GGAGGAGAGCAGTGTGCGGATGGTACCCGGCACACCCAGCCCTCAGAGACCTGAGTTCTT
CTGGCCACGTGGAACCTCGAACCCGAGCTCTGCAGAAGTGGCCCTGGAGATTGAGGGTCCC
TGGACACTCCCTATGGAGATCCGGGGAGCTAGGATGGGAACCTGCCACAGCCAGAAC
GGGCTGGCCCCAGGCAGCTCCAGGGGTAGAACGCCCTGTGCTTAAGACACTCCCTGCTG
CCCCGTCTGAGGGTGGCGATTAAAGTTGCTTC

FIGURE 46

MSGGWMAQVGAWRTGALGLALLLGLGLGLEAAASPLSTPTSAQAGPSSGCPPTKFQCR
TSGLCVPLTWRCRDLDCSDGSDEEECR1EPCTQKGQCPPPPGLPCPCTGVSDCSGGTDKKL
RNCSRLA克莱LRTLSDDC1PLTWRCRDLDCSDGSDEEECR1EPCTQKGQCPPPPGLPCPCTGVSDCSGGTDKKL
LESVTSLRNATTMGPPTVTLESVPSVGNATSSAGDQSGSPTAYGVIAAAAVLSASLVTATLL
LLSWLRAZERLRLPGLLVAJKESLLLSEQKTSLP

Signal sequence:

amino acids 1-30

Transmembrane domain:

amino acids 230-246

N-glycosylation site.

amino acids 126-130, 195-199, 213-217

Casein kinase II phosphorylation site.

amino acids 84-88, 140-144, 161-165, 218-222

N-muristoxylation site.

amino acids 3-9, 10-16, 26-32, 30-36, 112-118, 166-172, 212-218, 224-230, 230-236, 263-269

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 44-55

Leucine zipper pattern.

amino acids 17-39

FIGURE 47

CCCCACGCGTCGGTCTCGCTCGCGCAGCGCGGGCAGCAGAGGTCGCGCACAGATGCGG
GTTAGACTGGCGGGGGAGGAGGCGGAGGGAGGAAGGAAGTGCATGCATGAGACCCACAGA
CTCTTGCAGCTGGATGCCCTCTGTGGATGAAAGATGATCATGGAATGAACCCGAGCAATG
GAGATGGATTCTAGAGCAGCAGCAGCAGCAGCAACCTCAGTCCCCCAGAGACTCTTG
GCCGTGATCCTGTGGTTCACTGGCGCTGTGCTCGGCCCTGCACAGCTCACGGCGGGTT
CGATGACCTTCAGTGTGCTGACCCCGCATTCCCGAGAATGGCTTCAAGGACCCCCAGCG
GAGGGGTTTCTTGAGGGCTCTGTAGCCGATTCACTGCCAAGACGGATTCAAGCTGAAG
GGCCTACAAAGAGACTGTGTTGAAGCATTAAATGGAACCCTAGGCTGGATCCAAAGTGA
TAATTCCATCTGTGCAAGAAGATTGCCGTATCCCTAAATCGAAGATGCTGAGATTCTATA
ACAAGACATATAGACATGGAGAGAAGCTAACTCATCACTGTGATGAAGGATTCAAGATCCG
TACCCCGACCTACACAATATGGTTCTTATGTCGCGATGATGGAACGTGGATAATCTGCC
CATCTGCAAGGCTGCCGTGAGACCTCTAGCCTCTTCAATGGCTATGTAACACATCTGAGC
TCCAGACCTCCTCCGGGGACTGTGATCTCTATCGCTGCTTCCGGATTAAACTT
GATGGGCTCGGTATCTGAGTGCTACAAAACCTTATCGTGTGCTCAGCCCCACCCGGTG
CTTGCTCTGGAAGGCCAACGCTGTCACCTCAATGGTAGTGACTCGGAGATTCTGCT
GCCACCCGGGCCCTGTGAGCGCTAACACACCGGAACTGTGGTAGCTTACTGCGATCCT
GGCTACAGCCTCACCAAGCGACTACAAGTACATCACCTGCCAGTATGGAGAGTGGTTCC
TTATCAAGTCACTGCATCAAATCAGCAACAGTGGCCCGACCCATGAGACCCCTCTGA
CCACGTGGAAGATTGTGGCGTACGGCAACCAAGTGTGCTGGTGTGCTGCTCGTCATC
CTGGCCAGGATGTTCAAGGCCCCACTTCCCCCAGGGGGCCTCCCGAG
TTCCAGCAGTGAACCTGACTTGTGGTAGACGGCGTGCCTCATGCTCCGTCTATG
ACGAAGCTGTGAGTGGCGGGTTGAGTGCCTTAGGCCGGGTACATGCCCTCTGTGGCCAG
GGCTGCCCTTACCGTGGACGACCAGAGCCCCCAGCATACCCCGGCTCAGGGACACGGA
CACAGGCCAGGGAGTCAGAAACCTGTGACAGCGTCTCAGGCTCTTGAGCTGCTCCAAA
GTCTGTATTCAACCTCCAGGTGCCAAGAGAGCACCCACCCGTCTCGGACAACCCGTACATA
ATTGCCAGCACGGCAGAGGGGTGGCATCACCAGGCCAGGCATCCATCATGCCACTGGT
GTTGTTCTAAGAAACTGATGATTAAAAAATTCCAAAGTGTCTGAAGTGTCTCTCAA
ATACATGTTGATCTGGAGGTGATTCTTCTCTCTGGTTTAGACAAATGTAACAA
AGCTCTGATCCTTAAATTGCTATGCTGATAGAGTGGTAGGGCTGGAAAGCTTGTACAGTC
CTGTTCTCTGACACAGACTGATTAAAAATTAAAGNAAAAAA

FIGURE 48

MYHGMNPSNGDGFLQQQQQQPQSPQRLLAVILWFQLALCFGPAQLTGGFDDLQVCADPGI
PENGFRTPSGGVFFEGSVARFHQCQDGFKLKAGATKRLCLKHFNGTLGWIPSDNSICVQEDCRI
PQIEDAEIHNKTYRHGEKLIITCHEGFKIRYPDLHNMVSLCRDDGTWNNLPICQGCLRPLAS
SNGYVNISELQTSFPVGTVISYRCFPFGFKLDGSAYLECLQNLIWSSSPRCLALEAQVCPLP
PMVSHGDFVCHPRPCERYNHGTVEFYCDPGYSLTSFYKITYCQYGEWFPSYQVYCIKSEQT
WPSTHETLLTWKIVAFATSVLLVLLVILARMFQTKFKAHFPPRGPPRSSSDPDFVVVD
GVPVMLPSYDEAVSGGLSALGPGYMASVGQGCPPLVDDQSPPAYPGSGD'TDTGPGESETCDS
VSGSSELLQSLYSPPRCQESTHPASDNPDIIASTAEEVASTSPGIHHAHWVLFLRN

0002615.0001

Signal sequence:

amino acids 1-41

Transmembrane domain:

amino acids 325-344

N-glycosylation site.

amino acids 104-108, 134-138, 192-196

Casein kinase II phosphorylation site.

amino acids 8-12, 146-150, 252-256, 270-274, 313-317, 362-366,
364-368, 380-384, 467-471, 468-472

N-myristoylation site.

amino acids 4-10, 61-67, 169-175, 203-209, 387-393, 418-424,
478-484

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 394-405

FIGURE 49

CCCCACGCGTCCGCTCCGCGCCCTCCCCCCCACGCTCCGTGCGGTCCGTCGGTGGCCAGAGA
TGCTGCTGCCGCGGTTGCAAGTGTGCGCAGCAGCTCTGCCCGCAGCCGCTCAGCGCCGT
AGCGCCCGAGTGTGGGGGGCGCACCGCAGTCGGCCATGAGGCGGGAAACCGCGCTACAGG
CCGTGCTGCTGGCGTGTGCTGGTGGGCTGCGGGCCGACGGGTCGCTGCTGAGTCC
TCGGATTGGACCTCAGAGGAGGGCAGCCAGTCTGGGGGAGGGACACAGAGGCCTGTTA
TAAAGTCATTTACTTCATGATACTTCTCGAAGACTGAACCTTGAGGAAGCCAAAGAGCCT
GCAGGAGGGATGGAGGCCAGCTAGTCAGCATCGAGTCTGAAGATGAACAGAAACTGATAGAA
AAGTTCATGAAAACCTCTGCCATCTGATGGTGAACCTCTGGATTGGCTCAGGAGGCCTGA
GGAGAACAAAGCAATAGCACAGCCTGCCAGGACCTTATGCTGGACTGATGGCAGCATAT
CACAAATTAGGAACTGGTATGCGATGAGCGTCTCGGGCAGCGAGGTCTGGTGGTCATG
TACCATCAGCCATCGCACCCGCTGGCATCGGAGGCCCTACATGTTCCAGTGAATGATGA
CCGGTGAACATGAAGAACATTCTATTGCAATATTCTGATGAGAACCCAGCAGTTCTT
CTAGAGAAGCTGAAGGTGAGGAAACAGAGCTGACAACACCTGTACTTCCAGAAGAACACAG
GAAGAAGATGCCAAAAAAACATTAAAGAAAGTAGAGAACGCTGCCATGAAATCTGGCTACAT
CCTAATCCCAGCATCCCCCTCTCCTCTTGTGGTCAACAGTTGATGTTGGTTT
GGATCTGTAGAAAAAGAAAACGGGAGCAGCCAGACCCCTAGCACAAAAGCAACACACCATC
TGGCCCTCTCCTCACCAAGGGAACAGCCGGACCTAGAGGTCTAACATGTCATAAGAAAACA
AAGCGAAGCTGACTTAGCTGAGACCCGGCAGACCTGAAGAATATTCTCCAGTGTGTT
CGGGAGAAGCACTCCGATGACATGCTTGTGACTATGACAACATGGCTGTGAACCCATCA
GAAAGTGGTTGTGACTCTGGTGAAGCTGGAGAGTGGATTGTGACCAATGACATTATGAG
GTTCTCCCAGACCAATGGGGAGGAGTAAGGAGTCTGGATGGGTGAAAATGAAATATATG
GTTATTAGGACATATAAAACTGAAACTGACAACATGGAAAAGAAATGATAAGCAAATC
CTCTTATTTCTATAAGGAAAATACAGAAGGTCTATGAAACAAGCTTAGATCAGGCTCTG
GGATGAGCATGTGGTCCCCACGACCTCTGTTGGACCCCCACGTTTGGCTGTATCCTTTAT
CCCAGCCAGTCATCCAGCTGACCTTATGAGAAGGTACCTTGCCAGGTCTGCCACATAGTA
GAGTCTCAATAAAATGTCATTGGTTGGTGTATCTAACCTTAAGGGACAGAGCTTACCTG
GCAGTGTAAAGATGGGCTGTGGAGCTGGAAAACCCACCTCTGTTTCTGCTCTATAACAG
CAGCACATATTATCATACAGACAGAAAATCCAGAATCTTCAAAGGCCACATATGGTAGCACAG
GTTGGCCTGTGCATCGCAATTCTCATATCTGTTTTCAAAGAATAAAATCAAATAAAGA
GCAGGAAAAAA

FIGURE 50

MRPGTALQAVLLAVLLVGLRAATGRLLSASDDLRLGGQPVCRGQTQRPCYKVIYFHDTSRRL
NFEAAKEACRRDGGQLVSIESEDEQKLIKEKFIENLLPSDGDFWIGLRRREEKQSNSTACQDL
YAWTDGSISQFRNWWYVDEPCGSEVCVVMYHQPSAPAGIGGPYMFQWNDRNCNMKNNFICKY
SDEKPAVPSREAEGEETELTPVLPEETQEEDAKKTFKESREAALNLAYILIPSIPLLLLLV
VTTVVCWVWICRKRKREQPDSTKKQHTIWPSPHQGNSPDLEVNVIRKQSEADLAETRPDL
KNISFRVCVCSGEATPDDMSCDYDNMAVNPSSESGFVTLVSVEGFVTNDIYEFSPDQMGRSKES
GWENEIYGY

Signal sequence:

amino acids 1-21

Transmembrane domain:

amino acids 235-254

N-glycosylation site.

amino acids 117-121, 312-316

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 296-300

Casein kinase II phosphorylation site.

amino acids 28-32, 30-34, 83-87, 100-104, 214-218, 222-226,
299-303, 306-310, 323-327

N-myristoylation site.

amino acids 18-24, 37-43, 76-82, 146-152

01903615
071001

FIGURE 51

GGGGTCTCCCTCAGGGCCGGGAGGCACAGCGTCCCTGCTGAAGGGCTGGATGTACGC
ATCCGCAGGGTCCCGCGGACTTGGGGCGCCCGCTGAGCCCCGGCGCCCGAGAAGACTTGT
GTTTGCCTCCTGCAGCCTCAACCGGAGGGCAGCAGGGCTTACCAATGATCACTGGTGT
GTTCAGCAGTCGCTTGTGGACCCAGTGGCGTCTGACCTCGCTGGCGTACTGCCTGCACC
AGCGCGGGTGGCCCTGGCGAGCTGCAGGAGGCCATGCCAGTGTCCGGTGCACCGCAGC
CTGCTGAAGTTGAAAATGGTGCAGGTCTGTGTTGACACGGGCTCGGAGTCTCTCAAGCC
GCTCCCGCTGGAGGAGCAGGTAGAGTGGAAACCCCCAGCTATTAGAGGTTCCACCCAACTC
AGTTTGATTACACAGTCACCAATCTAGCTGGTGGTCCGAAACCATATTCTCCTTACGACTCT
CAATACCATGAGACCACCCCTGAAGGGGGCATGTTGCTGGCAGCTGACCAAGGTGGCAT
GCAGCAAATGTTGCTTGGAGAGAGACTGAGGAAGAACTATGTTGAGACATTCCCTTC
TTTCACCAACCTCAACCCACAGGAGGTCTTATTCTGTTCCACTAACATTTCGGAATCTG
GAGTCCACCCGTGTTGCTGGCTGGCTTCCAGTGTCAAGAAAGAAGGCCATCATCAT
CCACACTGATGAAGCAGATTCAAAGTCTGTATCCAACTACCAAAAGCTGCTGGAGCCTGA
GGCAGAGAACCCAGAGGCCGGAGGCAGACTGCCCTTTACAGCCAGGAATCTCAGAGGATTG
AAAAAGGTGAAGGACAGGATGGCATTGACAGTAGTGATAAAAGTGGACTTCTCATCCCT
GGACAACTGGCTGCCAGCAGGCACACAACCTCCCAAGCTGCCCATGCTGAAGGAGATTG
CACGGATGATCGAACAGAGAGCTGTGGACACATCCTGTACATACTGCCAAGGAAGACAGG
GAAAGTCTCAGATGGCAGTAGGCCATTCCACATCTAGAGAGCAACCTGCTGAAAGC
CATGGACTCTGCCACTGCCCGACAAGATCAGAAAGCTGTATCTCTATGCCGCTCATGATG
TGACCTTCATACCGCTTAAATGACCTGGGATTTTGACCAAAATGCCACCGTTGCT
GTTGACCTGACCAGTGAACATTACCAAGCCTGGAAATCTAAGGAGTGGTTGTGCAGCTCTA
TTACCACGGGAAGGAGCAGGTGCCAGAGGTTGCCCTGATGGGCTCTGCCGCTGGACATGT
TCTTGAATGCCATGTCAAGTTACCTTAAGGCCAGAAAAATACCATGCACTCTGCTCTCAA
ACTCAGGTGATGGAAGTTGGAAATGAAGAGTACTGATTATAAAAGCAGGATGTGTTGATT
TTAAAATAAAAGTGCCTTATACAATG

FIGURE 52

MITGVFSMRLWTPGVVLTSLAYCLHQRRVALAELQEADGQCPVDRSLLKLMVQVVFRHGAR
SPLKPLPLEEQVEWNPNQLLEVPPQTQFDYTVTNLAGGPKPYSYDSQYHETTLKGGMFAGQL
TKVGMQQMFALGERLRKNYVEDIPFLSPTFNPQEVFIRSTNIFRNLESTRCLLAGLFQCQKE
GPIIIHTDEADSEVLYPNYQSCWSLRQRTRGRQTASLQPGISEDLKKVKDRMGIDSSDKD
FFILLDNVAAEQAHNLPSCPMLKRFARMIEQRAVDTSLYILPKEDRESLQMAVGPFLHILES
NLLKAMDSATAPDKIRKLYLYAAHDVTFIPLLMTLGIFDHKWPFFAVDLTMELYQHLESKEW
FVQLYYHGKEQVPRGCPDGLCPIDMFLNAMSVTLSPEKYHALCSQTQVMEVNEE

Signal sequence:

amino acids 1-23

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 218-222

Casein kinase II phosphorylation site.

amino acids 87-91, 104-108, 320-324

Tyrosine kinase phosphorylation site.

amino acids 280-288

N-myristoylation site.

amino acids 15-21, 117-123, 118-124, 179-185, 240-246, 387-393

Amidation site.

amino acids 216-220

Leucine zipper pattern.

amino acids 10-32

Histidine acid phosphatases phosphohistidine signature.

amino acids 50-65

FIGURE 53

CTCTCTTAAACATACTGAGCTAAACTAAATATTGCTGCTGGGACCTCCTTAGCCT
TAAATTTAGCTCATCACCCTCACCTGCTGGTCAATGGCTCTGCTATTCTCCTTGATCCTT
GCCATTGACCAAGACCTGGATTCTCTAGCGCTCCATCTGGAGTGGCTGGGGGGCCT
CCACCGCTGTGAAGGGCGGGTGGAGGGAACAGAAAGGCCAGTGGGACCGTGTGATG
ACGGCTGGACATTAAGGACGTGGCTGTGTTGCCCCGAGCTGGCTGTGGAGCTGCCAGC
GGAAACCCCTAGTGGTATTGATGAGGCCACAGCAGAAAAAGAGCAAAAGGCTCATCCA
ATCAGTCAGTTGCACAGGAACAGAACAGATACTGGCTCAGTGTGAGCAAGAACAGTTATG
ATTGTTACATGATGAAGATGCTGGGCATCGTGTGAGAACCCAGAGAGCTTTCTCCCCA
GTCCCCAGAGGGTGTCAAGGTGGCTGACGGCCCTGGCATTGCAAGGGACCGTGGAAAGTGA
GCACCCAGAACCAAGTGGTATACCGTGTGCCAGACAGGTGGAGCCTCCGGGCGAACAGGTGG
TGTGCCGCAGCTGGATGTGGAGGGCTGTACTGACTCAAAACGCTGCAACAAGCATGCC
TATGGCCGAAACCCATCTGGCTGAGCCAGATGTCAGTCAGGACGAGAACGAAACCCCTCA
GGATTGCCCTCTGGGCTTGGGGAAAGAACACCTGCAACCATGATGAAGACACGTGGTGC
AATGTGAAGATCCCTTGACTTGAGACTAGTAGGGAGAGAACACCTGCTCTGGGCGACTG
GAGGTGCTGCACAAGGGCGTATGGGCTCTGTCTGTGATGACAACCTGGGAGAAAAGGAGGA
CCAGGGTGTATGCAAGCAACTGGGCTGTGGGAAGTCCTCTCCTCCCTCAGAGACCGGA
AATGCTATGCCCTGGGTTGGCCGCATCTGGCTGGATAATGTTGCTCAGGGAGGAG
CAGTCCCCTGGAGCAGTGCAGCACAGATTGGGGTTTCAGACTGCACCCACAGGAAGA
TGTGGCTGTCATCTGCTCACTGTAGGTGGCATCATCTAATCTGTTGAGTGGCTGAATAGAA
GAAAAACACAGAACAGAAGGGAGCATTACTGTCACATGACTGCATGGGATGAACACTGATCT
TCTTCTGCCCTGGACTGGACTTATACTTGGTCCCCCTGATTCTCAGGCTTCAGAGTTGG
ATCAGAACATTACAACATCAGGTCTAGTCTCAGGCCATCAGACATACTGGAAACTACATCA
CCACCTTCTATGTCACATTGACACAGCAGATCCAGCCTCCATAATTGTTGAT
CAACTACTTAAACATTCTCATA
CACCAATTGTCCTGTTCTCTGAAGAACCTGACAAAATACAGATTGGTACTGAAAGAGA
TTCTAGAGGAACGGAATTAAAGGATAAAATTCTGAATTGGTTATGGGTTCTGAAATTG
GCTCTATAATTCTAATTAGATATAAAATTCTGGTAACCTTATTACAATAATAAGATAGCAC
TATGTTGTCAAA

FIGURE 54

MALLFSLILAICTRPGFLASPGVRLVGGHLRCEGRVEVHQKGQWGTVCDDGWDIKDVAVLC
RELGCAGAASGTPSGILYEPPAEKEQKVLIQSVSCTGTEDTLAQCEQEEVYDCSHDEDAGASC
ENPESSFSFSPVPEGVRLADGPGHCKGRVEVKHQNQWYTVQGTGWSLRAAKVVCRQLGCGRAVL
TQKRCNKHAYGRKPIWLSQMCSGREATLQDCPSGPWGKNTCNHDEDTWVECEDPFDLRLVG
GDNLCGSRLEVHLKGVWGSVCDDNWGEKEDQVVKQLGCGKSLSPSFRDRKCYGPGVGRIDL
DNVRCSGEEQSLEQCQHRFWGFHDCTHQEDAVICSV

Signal sequence:

amino acids 1-15

Casein kinase II phosphorylation site.

amino acids 47-51, 97-101, 115-119, 209-213, 214-218, 234-238,
267-271, 294-298, 316-320, 336-340

N-myristoylation site.

amino acids 29-35, 43-49, 66-72, 68-74, 72-78, 98-104, 137-143,
180-186, 263-269, 286-292

Amidation site.

amino acids 196-200

Speract receptor repeated domain signature.

amino acids 29-67, 249-287

00902615-071001

FIGURE 55

ACTGCACTCGGTTCTATCGATTGAATTCCCCGGGGATCCCTCTAGAGATCCCTCGACCTCGAC
CCACCGCGTCCCGGGACCGTGGGGCGGACCGCGTGGGCCGGTACCCAGGAAGAGTCTGCCAAG
GTGAAGGCCATGGACTTCATCACCTCCACAGCCATCCTGCCCTGCTGTTGGCTGCCGG
CGTCTTCGGCCTTCCGGCTGCTGCAGTGGGTGCGCGGAAGGCCAACCTGCCGAATGCTG
TGGTGGTATCACAGGCCACCTCAGGGCTGGGAAAGAATGTGAAAGTCTTCTATGCT
GCCGGTGCTAAACTGGTGCTCTGTGGCCGAATGGTGGGCCCTAGAACAGCTCATCAGAGA
ACTTACCGCTTCTCATGCCACCAAGGTGCAAGACACACAAGCCTACTTGGTGACCTTCGACC
TCACAGACTCTGGGCCATAGTTGCAGCAGCAGCTGAGATCCTGCAGTGCTTGCTATGTC
GACATACTTGTCAACAATGCTGGGATCAGCTACCGTGGTACCATCATGGACACCACAGTGA
TGTGGACAAGAGGGCATGGAGACAAACTACTTGGCCAGTTGCTCTAACGAAAGCACTCC
TGCCCTCCATGATCAAGAGGGCAAGGCCACATTGTCGCCATCAGCACGATCCAGGGCAAG
ATGAGCATTCTTTCTGATCAGCATATGCAGCCTCAAGCACGCAACCCAGGCTTCTTGA
CTGTCTGCGTGGCGAGATGGAACAGTATGAAATTGAGGTGACCGTCACTAGCCCCGGCTACA
TCCACACCAACCTCTGTAAATGCCATACCGGGATGGATCTAGGTATGGAGTTATGGAC
ACACACACAGCCCCAGGGCGGAAGCCCTGTGGAGGTGCCAGGATGTTCTGCTGCTGTGGG
GAAGAAGAAGAAGATGTGATCCTGGCTGACTTACTGCCTCTGGCTTTATCTTGAA
CTCTGGCTCCTGGCTTCTCAGCCTCATGGCTCCAGGGCCAGAAAAGAGCGGAAATCC
AAGAAACTCCTAGACTCTGACCAGCCAGGGCAGGGCAGAGAACGAGCACTTTAGGCTTGC
TTACTCTACAAGGGACAGTTGCATTGTTGAGACTTAATGGAGATTGCTCACAAGTGGG
AAAGACTGAAGAAAACACATCTCGTGCAGATCTGCTGGCAGAGGACAATAAAAACGACAACA
AGCTTCTCCAGGGTGAGGGAAACACTTAAGGAATAATGGAGCTGGGTTAACACT
AAAAACTAGAAATAAACATCTCAAACAGTAAAAAAGGGCGCCGCACTCTAG
AGTCGACCTGCAGAAGCTTGGCCCATGGCCAACTTGTTATTGCAGCTTATAATGGTTAC

FIGURE 56

MDFITSTAILPLLGCLGVFGFLFRLLQWVRGKAYLRNAVVIITGATSGLGKECAKVFYAAGA
KLVLCGRNGGALEELIRELTASHATKVQTHKPYLVTFDLTDGAIVAAAAEILQCFGYVDIL
VNNAGISYRGТИMDTTVDKRVMETNYFGPVALTKALLPSMIKRRQGHIVAIISSIQGKMSI
PFRSAYAASKHATQAFFDCLRAEMEQYEIEVTVISPGYIHTNLSVNAITADGSRYGVMDTTT
AQGRSPVVAQDVLAAGKKKDVLADLLPSLAVYLRTIAPGLFFSLMASRARKERKSKNS

Signal sequence:

amino acids 1-21

Transmembrane domain:

amino acids 104-120, 278-292

N-glycosylation site.

amino acids 228-232

Glycosaminoglycan attachment site.

amino acids 47-51

Casein kinase II phosphorylation site.

amino acids 135-139, 139-143, 253-257

Tyrosine kinase phosphorylation site.

amino acids 145-153, 146-153

N-myristoylation site.

amino acids 44-50, 105-111, 238-244, 242-248, 291-297

Amidation site.

amino acids 265-269

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 6-17

FIGURE 57

CCACACGCGTCCGCTGGTGTAGATCGAGCAACCCCTCTAAAAGCAGTTAGAGTGGTAAAAAA
AAAAAAAAAACACACCAAAACGCTCGCAGGCCAAAAGGGATGAAATTCTCTGGACATCCCTC
CTGCTCTCCGTTACTGATCGTCTGCTCCCTAGACTCTCGTGAAGCTTTTATTCCCTAA
GAGGGAAAATCAGTCACCGGGCAAATCGTGTGATTACAGGAGCTGGCATGGAATTGGGA
GACTGACTGCCTATGAATTGCTAAACTAAAAGCAAGCTGGTCTCTGGGATATAAATAAG
CATGGACTGGAGGAAACAGCTGCAAATGCAAGGGACTGGGTGCAAAGGTTCATACCTTGT
GGTAGACTGCAGCAACCGAGAAGATATTACAGCTCTGCAAAGAAGGTGAAGGCAGAAATTG
GAGATGTTAGTATTAGTAAATAATGCTGGTAGTCTATACATCAGATTGTTGCTACA
CAAGATCCTCAGATTGAAAAGACTTTGAAAGTTAATGTTACTTGACATTTCTGGACTACAAA
GGCATTCTCTCGCAATGACGAAGAATAACCATGGCCATTGTCACTGTGGCTTCGGCAG
CTGGACATGTCCTGGCCCTCTTACTGGCTACTGTTCAAGCAAGTTGCTGCTGTTGGA
TTTCATAAAACTTGACAGATGAACGGCTTACAATAACTGGAGTCAAAACACATG
TCTGTGTCCTAATTCGTAACACTGGCTTACATCAAAATCCAAGTACAAGTTGGACCCA
CTCTGGAAACCTGAGGAAGTGGTAAACAGGCTGATGCATGGGATTCTGACTGAGCAGAAAGATG
ATTTTATTCCATCTTCTATAGCTTTTTAACACATTGAAAGGATCTTCTGAGCGTTT
CCTGGCAGTTTAAACGAAAATCAGTGTAAAGTTGATGCACTTATTGGATATAAAATGA
AAGCGCAATAAGCACCTAGTTCTGAAAACGTGATTTACCAAGGTTAGGTTGATGTCATCTA
ATAGTGCCAGAATTTAATGTTGAACCTCTGTTTCTAATTATCCCCATTCTCAATA
TCATTTTGAGGCTTGGCAGTCCTCATTTACTACCACTTGTCTTAGCCAAAAGCTGATT
ACATATGATATAAACAGAGAAAATACCTTAGGGTCAAGTTAAGGAAAATGAAGAAAAAGAA
CCAAAATGACTTTATTAATAATTTCCAAGATTATTTGTTGCTCACCTGAAGGCTTGCAA
AATTGTAACATAACCGTTTATTAACATATTTTATTGGATTGACTTAAATTGTTGT
ATAATTGTTGTTCTTTCTGTTCTACATAAAATCAGAAACTTCAGCTCTCTAAATAAAA
TGAAGGACTATATCTAGTGGTATTCACAATGAATATCATGAACTCTCAATGGTAGGTTTC
ATCCTACCCATTGCCACTCTGTTCTGAGAGATACTCACATTCCAATGCCAAACATTCT
GCACAGGGAAAGCTAGAGGTGGATACACGTGTGCAAGTATAAAAGCATCACTGGGATTAAAG
GAGAATTGAGAGAATGTACCCACAAATGGCAGCAATAATAATGGATCACACTTTAAAAAA
AA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 58

MKFLLDILLLPLLIIVCSLESFVKLFIPKRRKSVTGEIVLITGAGHGIGRLTAYEFAKLKSK
LVLWDINKHGLEETAACKCKGLGAKVHTFVVDCSNREDIYSSAKVKAEIGDVSILVNNAGVV
YTSDLFATQDPQIEKTFEVNLAHFWTTKAFLPAMTKNNHGHIVTVASAAGHVSVPFLLAYC
SSKFAAVGFHKTLTDEAALQITGVKTTCLCPNFVNTGFIKNPSTSLGPTLEPEEVVNRLMH
GILTEQKMFIPSSIAFLTTLERILPERFLAVLKRKISVKFDAVIGYKMKAQ

Signal sequence:

amino acids 1-19

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 30-34, 283-287

Casein kinase II phosphorylation site.

amino acids 52-56, 95-99, 198-202, 267-271

N-myristoylation site.

amino acids 43-49, 72-78, 122-128, 210-216

09902615-071001

FIGURE 59

CCACCGCGTCCGGACCGCGTGGGTCGACTAGTTCTAGATCGCGAGCGGCCGCCGGCTC
AGGGAGGAGCACCGACTGCGCCGCACCTGAGAGATGGTGGCATGTGAAGGTGATTG
TTCGCTGGTCTGTTGATGCCCTGGCCCTGTGATGGCTGTTCTCCCTATACAGAACT
GTTTCCATGCCACCTAAGGGAGACTCAGGACAGCCATTATTCCTACCCCTACATTGAAGC
TGGGAAGATCCAAGGAAGAGAAATTGAGTTGGCTGGCCCTTCCAGGACTGAACATGA
AGAGTTATGCCCTTCCCTACCGTGAATAAGACTTACACAGAACCTCTCTGGTC
TCCCCAGCTCAGATAACAGCAGAAGATGCCAGTAGTTCTGGCTACAGGGTGGGGCGG
AGGTTCATCCATGTTGGACTCTTGTGGAACATGGGCTTATGTTGTCAGTAACATGA
CCTTGCCTGACAGAGACTTCCCTGGACCACAAACGCTCTCATGCTTACATTGACATCCA
GTGGGCACAGGCTCAGTTTACTGTGATACCCACGGATATGCAATGAGGACGATGT
AGCACGGGATTATACTAGTGCACTAATTCACTTTCCAGATATTCTGAATATAAAAATA
ATGACTTTTATGACTGGGAGTCTTATGCGAGGAAATATGTCAGCCATTGACACCTC
ATCCATTCCCTAACCCCTGTGAGAGGAGGTGAAGATCAACCTGAACGGAAATTGCTATTGGAGA
TGGATATTCTGATCCCGAATCAATTATAGGGGCTATGAGAACATTCTGTACCAAATTGGCT
TGGTGGATGAGAACAAAAAAAGTACTTCCAGAAGCAGTGCCTGATGAATGACACATC
AGGAACGAGAACACTGGTTGGGCTTGAATACTGGATAACACTAGATGGCAGACTAAC
AAGTGATCCTTCTACTTCCAGAATGTTACAGGATGTAGAATTACTATACTTTGGCT
GCCAGGAACTCTGAGGATCAGCTTACTATGAAATTGGTCACTCCAGAGGTGAGACAA
GCCATCACGCTGGGAATCAGACTTTAATGGAAACTATAGTTGAAAAGTACTTGGAGA
AGATACAGTACAGTCACTGGCATGTTAAGCATGAAATCATGAAATAATTATAAGGTCTGA
TCTACAATGGCCAACTGGACATCATGTCAGCTGCCCTGACAGAGCGCTCTTGATGGC
ATGGACTGGAAAGGATCCCAAGGAAATCAAAGGGAGAAAAAAAGTTGGAAAGATCTTAA
ATCTGACAGTGAAGTGGCTGGTTACATCGGCAAGGGTGAACACTCCATCAGGTAATTATT
GAGGTGGAGGACATATTACCCATGACCAAGCCTCTGAGAGCCTTGTGACATGATTATCGA
TTCACTTATGGAAAAGGATGGGATCTTATGTTGGATAAACTACCTTCCAAAAGAGAACAT
CAGAGGTTTCATTGCTGAAAGAAAATCGTAAAACAGAAAATGTCATAGGAATAAAAAAA
TTATCTTTTCTATCTGCAAGATTTCATCAATAAAAATTATCCTGAAACAAAGTGAGC
TTTGTTTTGGGGGAGATGTTACTACAAAATTAAACATGAGTACATGAGTAAGAATTACA
TTATTTAACTTAAAGGAGTGAAGGTATGGATGTGACACTGAGACAAGATGTATAAATGA
AATTTTAGGGTCTGAAATAGGAAGTTTAAATTCTTAAGAGTAAGTGAAGGAGTGCAGTTG
TAACAAACAAAGCTGAAACATCTTCTGCCAATAACAGAAAGTGGCATGCCGTGAAGGT
GTTTGGAAAATATTGGATAAGAATAGCTCAATTATCCAATAAATGGATGAAGCTATAA
TAGTTTGGGGAAAAGATTCTCAAATGTATAAAGTCTTAAAGCAGAAAATTCTTGAATAA
AAAATATTATATAAAAAGTAAAAAA

FIGURE 60

MVGAMWKVIVSLLMPGCDGLFRSLYRSVSMPKGDSGQPLFLTPYIEAGKIQKGREL
SVPFPGLNMKSYAGFLTVNKTYNSNLFFWFFPAQIQPEDAPVVLWLQGGPGGSSMFGLFVEH
GPYVVTSNMTLDRDFPWTTTLSMLYIDNPVGTGFSFTDDTHGYAVNEDDVARDLYSALIQF
FQIFPEYKNNDVFVVTGESYAGKYVPAIAHLIHSLNPVREVKINLNGIAIGDGYSDPESIIGG
YAEFLYQIGLLDEKQKKYFQKQCHECIEHIRKQNWFEAFFEILDKLLDGLTSDP
SYFQNVVTGCSNYYNFRLRCTEPEDQLYYVKFLSLPEVRQAIHVGNQT
FNDGTTIVEKYLREDTVQSVKPWLT
EIMNNYKVLIYNGQLDIIVAAALTERSLMGMDWKGSQEYKKA
EKKVWKIFKSDSEVAGYI
RQAGDFHQVIIRGGGHILPYDQPLRAFDMINRFIYKGKWD
PYVG

Signal sequence:

amino acids 1-22

N-glycosylation site.

amino acids 81-85, 132-136, 307-311, 346-350

Casein kinase II phosphorylation site.

amino acids 134-138, 160-164, 240-244, 321-325, 334-338, 348-352,
353-357, 424-428

Tyrosine kinase phosphorylation site.

amino acids 423-432

N-myristoylation site.

amino acids 22-28, 110-116, 156-162, 232-238

Serine carboxypeptidases, serine active site.

amino acids 200-208

Crystallins beta and gamma 'Greek key' motif signature.

amino acids 375-391

1000 900 800 700 600 500 400 300 200 100 0

FIGURE 61

CGAGGGCTTCCGGCTCCGAATGGCACATGTGGGAATCCCAGTCTTGTGGCTACAAACAT
TTTCTCTTCTAAACAGTCTAACAGCTCTAACAGCTAGTGTACAGGGGTTCTTCTT
GCTGGAGAAGAAAGGGCTGAGGGCAGAGCAGGGCACTCTCACTCAGGGTGACCACCTCTT
CTCTCTGTGATAACAGAGCATGAGAAAGTGAAGAGATGCAGCGGAGTGAGGTGATGGAAG
TCTAAAATAGGAAGGAATTCTGTGCAATATCAGACTCTGGGAGCAGTTGACCTGGAGAGC
CTGGGGAGGGCTGCTAACACAGCTTCAAAAAACAGGAGCGACTTCCACTGGCTGGGAT
AAGACGTGCGGTAGGATAGGAAGACTGGTTAGTCTTAATATCAAATTGACTGGCTGGG
TGAACCTCAACAGCCTTTAACCTCTGTGGAGATGAAACGATGCTTAAGGGCCAGAAA
TAGAGATGCTTGTAAAATAAAATTTAAAAAAAGCAAGTATTATAGCATAAAGGCTAGA
GACCAAAATAGATAACAGGATCTCTGAACTCTCAAGAGGGAGAAGTATGTTAAAATA
GAAAACAAAATGCGAAGGAGGAGACTCACAGAGCTAACACCAGGATGGGACCTGGGTC
AGGCCAGCCTCTTGTCTCCCGGAAATTATTGTGCTGACACTCTGCTTGTGTTTT
GCAAAATCATGTGAGGGCAACGGGGAAAGGTGGAGCAGATGAGCACACACAGGAGCCGT
CCTCACCGCCGCCCTCTCAGCATGGAACAGAGGCAGCCCTGGCCCGGCCCTGGAGGTGG
ACAGCCGCTCTGTGGCTCTGCTCATGAGCTGGTCTGGGTCTGCTGGCCCCCAGCAGCCGGC
ATGGCTCATGTCAGCACCTTCACTCTGAGAATCTGTGACCTGGACCTTCAACCACTTGACCGT
CCACCAAGGGACGGGGCCGCTATGTGGGCCATCAACCGGGTCTATAAGCTGACAGGCA
ACCTGACCATCAGGTGGCTCATAAAGACAGGGCAGAAGAGGACAACAAGTCTCGTACCCG
CCCTCATCGTCAGGGCTGAGCAGGCTCACCCCTACCAAAATGTCACAAAGCTGCT
CATCATGACTACTCTGAGAACGCCCTGCTGGCTGTGGAGCCTTACCCAGGGGTCTGCA
AGCTGCTGCGGTGGATGACCTCTTCATCTGGTGGAGCCATCCCAAGAAGGAGCACTAC
CTGTCAGTGTCAAAAGACGGCACCATGTACGGGTGATTGTGCGCTCTGAGGGTGAGGA
TGGCAAGCTCTTCTATGGCAGGGCTGTGGAGTGGAAAGCAGGATTACTTCCGACCCCTGTCA
GCCGGAAAGCTGCCCGAGACCCCTGAGTCTCAGGCCATGCTCGACTATGAGCTACACAGGAT
TTTGTCTCTCTCATCAAGATCCCTCAGACACCCCTGGCCCTGGTCTCCCATTTGACAT
CTTCTACATCTACGGCTTGTGGTAGTGGGGCTTGTCTACTTCTCAGTGTCCAGGCCGAGA
CCCTGAGGGTGTGGCCATCAACTCCGCTGGAGACCTCTCTACACCTCACCATGTGCG
CTCTGCAAGGATGACCCCAAGTCCACTCATACGTGCTCTGCCCTCGGCTGACCCGGGC
CGGGGTGAATAACGGCTCTGCAAGGCTGTTACCTGGCCAAGGCTGGGACTCACTGGCC
AGGGCTTCAATATCACCAGGCCAGGACGATGTACTCTGCCCCATGTCGCTTCCATCAGG
CACTTCAAGGATCAAGGAGCCCTGCACTCTGTAACCAAGGGCAGGGCAACCTGGAGCTCAACTGGC
TGCTGGGAAGGAGCTTCACTGGCAAGGCTGCAAGGGCCCTGCCCCATCGATGATAACTTCTGTGA
CTGGACATCAACCGCCCTGGAGGCTCAACTCCAGTGGAGGGCTGACCCCTGTACACCCAC
CAGCAGGGACCGCATGACCTCTGTGGCCTCTACGTTAACAGGCTACAGCGTGGTTTTG
TGGGACTAAGAGTGGCAAGGCTGAAAAAAAGGTAAGAGTCTATGAGTTCAAGTGTCCAATGCC
ATTCACTCTCAGCAAAGAGTCCCTCTTGAAGGTAGCTATTGGTGGAGATTTAACTATAG
GCAACTTATTTCTGGGAACAAAGGTGAATGGGGAGGTAAAGAAGGGTTAATTGTG
ACTTAGCTCTAGCTACTTCCAGCCATCAGTCATTGGGTATGTAAGGAATGCAAGCGTA
TTCAATATTCCCAAATTTAAGAAAAAACTTAAAGAAGGTACATGCAAAAGCAAA

FIGURE 62

MGTLGQASLFAPPGNYFWSDHSALCFAESCEGQPGKVEQMSTHRSRLITAAPLSMEQRQPWP
RALEVDSDRSVVLSSVVVLLAPPAAGMPQFSTFHSENRDWTFNHLTvhQGTGAVYVGAINRV
YKLTGNLTIQVAHTGPEEDNKSRYPPLIVQPCSEVLTLNNVNKLLIIDYSENRLLACGSL
YQGVCKLLRLDDLFILVEPSHKKEHYLSSVNKTGTMYGVIVRSEGEDGKLFIGTAVDGKQDY
FPTLSSRKLPRDPESSAMLDYELHSDFVSSLIKIPSDTLALVSHFDIFYIYGFAASGGFVYFL
TVQPETPEGVAINSAAGDLFYTSRIVRLCKDDPKFHSYVSLPFGCTRAGVEYRLLQAAYLAKP
GDSLQAQAFNITSQDDVLFAIFSKGQKQYHHPDDDSALCAFPIRAINLQIKERLQSCYQGEGN
LELNWLLGKDVQCTKAPVPIDDNFCGLDINQPLGGSTPVEGLTLYTTSRDRMTSVASYVYNG
YSVVFGTSGKLKKVRVYEFRCSNAIHLLSKESLLEGSYWWRFNYRQLYFLGEQR

TRIGLYCIDE GLYCEROL
TRIGLYCIDE GLYCEROL
TRIGLYCIDE GLYCEROL
TRIGLYCIDE GLYCEROL
TRIGLYCIDE GLYCEROL

Signal sequence:

amino acids 1-32

Transmembrane domain:

amino acids 71-87

N-glycosylation site.

amino acids 130-134, 145-149, 217-221, 381-385

Casein kinase II phosphorylation site.

amino acids 139-143, 229-233, 240-244, 291-295, 324-328, 383-387,
384-388, 471-475, 481-485, 530-534

N-myristoylation site.

amino acids 220-226, 319-325, 353-359, 460-466, 503-509

FIGURE 63

AGGCTCCCGCGCGGGCTGAGTCGGACTGGGAAACCGGGTCCCGCGCTTAGAGAACACCGCGATGACCA
CGTGGAGCCTCCCGCGAGGCCCGCCACGCTGGACTCTCTGCTGGTGTCTGGGCTTCCTGGTGTCTCC
GCAGGCTGACTGGAGCACCCCTGCTGCCCTCGGCCATCGAACAGCTGGGGCTCAGGCCAAGGGCTGGA
ACTCTATGCTGGAGGATTCACCCCTCTGGATCTCGGGGCTCCATCAGTCTTCCGTTGGCCAGGGAGTACT
GGAGGGACCGCCTGCTGAAGATGAAGGCCCTGTGGCTTAACACCTTACACCCACTATGTTCGTTGGACACTGATCG
AGCCAGAAAGGCCAAATTGAGCTCTCTGGAGGCCCTTGCTGGAGGCCCTCGTGTCTGATGGCCCGAACAGAGATCG
GGCTGTGGGTGATTCTCGCTCGAGCCCCCTACATCTGAGTGAATGGACCTCGGGGGCTTGCCCACTGCGCTAC
TCCAAGACCCCTGGCATGAGGCTGAGGACAACCTAACAGGCTTACCGAAGCAGTGAGCTTATTTGACCACC
TGATGTCCAGGGTGGTCACTTCAAGTGAACGCTGGGGGACTATCTGGCGTGAAGGAGGGATGAAATATG
GTTCTATAATAAGACCCCGCATACATGCCCTAGCTCAAGAGGACTGGAGGACGGTGGCATTTGGAACCTGC
TCTGACTCTAGACAAACAGGATGGCTGAGGGGATTTGCTGGGAGACTTACACTTGCACT
CAACACAGGGCTGCACTGACTGACCACTTCTCTCAACCTCTCAGGGACTCAGCCAAAGATGTGATGGAGT
ACTGGACGGGAAATTTGAGCTCTCTGGAGGCCCTCAAAATATCTTGATTCTCTGAGGTTTTGAAAACCGTGT
CTGGCATTGAGCAGCCGGCTCTCCATCAACCTCTAATGTCCTGGACAGGACCAACTTGGCTTCATGAATG
GAGCCATGCACTTCATGACTACAAGTCAAGATGTCAACAGCTAGACTATGATGCTGTCTGACAGAACGGGG
ATTACACAGGAAAGTACATGAAGCTTGAGGACTCTTGGGCTCATCTGGGACCCCTAACCTGAGCT
ACCTCTTCCAAAGGCTTATGAGGCTTAAAGCCCTAAGCCGACTCTGTACTCTGCTCTGTGGAGGCCCTCAAGTACC
TGGGGAGGAAATCAAGTCTGAAAGGCCATCATGGAGAACCTGGCAGTCAATGGGGAAATGGACAGTCT
TCGGGATCATCTCATGAGCACAGCATCTCTGCTCTGCTCATGTCAGTGGCCATGATCGGGGAG
TCTGGTGTGAAACAGTATCCATAGGATTCTGGACTACAAGAACAGAAGATGCTGTCCTCATGCAAGGGTT
ACACCGTCTGAGGGACTTGGTGGAGGATCTGTTGGGAGACTGGAGGCTCAACTTGGGGAAATATTGATGACCGGGCCTAACAG
GCTTAATTGGAAATCTTATCTGAATGCTTACCTGGCAAAACTTCAAGAATCTATAGCTCTGGATATGAAGAAGA
GCTCTTCTTCAAGGGGACTTGGGCTTCCCTGGGAAATGGNCTTCCCTGGAGAACACCCACATTACCTGCTTCTCTGG
TCTGGTGTGCTCATGCTTCAACGGCTTGTGACACCTTCTGAAGCTGGGGCTGGAGAAGGGGTTGTATTCA
TCAATGGCCAGAAGCTTGGAGCTTGGAGAATTTGAGACCCCCAGAGGCTTACCTCCAGGTCCCTGGTGA
GCAGCGGAATCACAGGTCTGCTTGTGAGGAGACATGGCCGGGCCCTGCAATTACAGTCAAGGAAACCCCC
ACCTGGCAGGAACAGTACATTAAGTGAAGGGCTGGGACCCCCCTCTGCTGTGCTGAGGAACTGGGGCTTC
CTCTGGCTGAGGAGCTGGCTGGCTGGCCACCCCTCAGTCAAGGAAAGGGGGATCTGCTGGCTGGGGCTTC
ACTGGGGGCTCAAGTCTGCCCCCTGTCTCAGTCAAAACCTAAGGCTGAGGGAAAGGGGGATGGCTCTGGGG
TGGCTTGTGTGATGAGGGCTTCTACAGGCCCTGCTCTGTGCCCAGGGTGTGGGCTGTCTCTAGGGTGGGAGC
AGCTAATCAGATGCCAGGCCCTTGGGCTTGGGAGGCCATCTGGGAGGCCATCTGGGAGGCCATCTGGGAGC
TGGGAGCATCTGTTGACTCAGGGCTGCTTGTGCTGGGAGGCCATCTGGGAGGCCATCTGGGAGGCCATCTGGGAGC
TTATCCCGAAATCTGGGTGCTGACAGTGTAGAGGGTGGGGAGGGGTGCTCACTGAGCTGACTTTGTT
CTCCCTTCAACACCTCTGAGCTTCTTGGGATCTCTGGAGAACACTGGCTGAGAACACATGTGACTTCCCTT
TCCCTTCCCACTCGCTGCTTCCCAACAGGGTGAAGGGCTGGGCTGGAGAACAGAAATCTTACCCCTGGCTCTCC
CAAGTTAGCTGGGAGCTCTGGTGTCTAGTGGAGGGAGCATGTGAGTCTGGCAGAGGCCATGGGCCATGTCTGCA
CATCCAGGGAGGGAGACAGAACGGCCAGCTCACATGTGAGTCTGGCAGAGGCCATGGGCCATGTCTGCA
AGGGAGGGAGGAGACAGAACGGCCAGCTCACATGTGAGTCTGGCAGAGGCCATGTCTGCA
GGAGGAGCACAGGCCAGCTCACATGTGAGTCTGGCAGAGGCCATGGGCCATGTCTGCA
ACAGAACGGCCAGCTCACATGTGAGTCTGGCAGAGGCCAGCTCACATGTGAGTCTGGCAGAGGCCAGCTGGC
GAAGTGTGTCAGTCCGCAATTGAGCTTGTGTTCTGGGGCCAGGCCAACACTGGCTTGGGCTACTGTCTG
GTTGAGCTAAAGCTATAACCTGAACTACRA

FIGURE 64

MTTWSLRRRPARTLGLLLLVLGFLVRLRDWSTLVPLRLRHQLGLQAKGWNFMLEDSTFW
IFGGSIHYFRVPREYWRDRLLKMKACGLNTLTTYVPWNLHPERGKFDPSGNLDLEAFVLMA
AEIGLWVILRPGPYICSEMDLGGLPSWLLQDPGMRLRTTYKGFTEAVIDLYFDHLMRSVVPLQ
YKRGGPIIAVQVENEYGSYNKDPAYMPYVKALEDRGIVELLLTSNDNKGLSKGIVQGVLAT
INLQSTHELQLLTTFLFNVQGTQPKMVMEYWTGWFDSWGPHNILDSEVLKTVSAIVDAGS
SINLYMFHGGTNFGFMNGAMHFDYKSDVTSYDYDAVLTEAGDYTAKYMKLRDFFGSISGIP
LPPPPDLPKMPYEPPLTPVLYSLWDALKYLGEPIKSEKPINMENLPVNNGNGQSFQGYILYE
TSITSSGILSGHVVHDRVQVFVNTVSIGFLDYKTTKIAVPLIQGYTVRLVRLVENGRVNVYGEN
IDDRRKGLIGNLYLNDSPKLNFRYISLDMKKSFFQRFGLDKWXSLPETPTLPAFFLGLSIS
STPCDTFLKLEGWEKGVVFINGQNLGRYWNIGPQKTLVLPGPWLSSGINQVIVFEETMAGPA
LQFTETPHLGRNQYIK

Signal sequence:

amino acids 1-27

Casein kinase II phosphorylation site.

amino acids 141-118, 253-257, 340-344, 395-399, 540-544, 560-564

N-myristoylation site.

amino acids 146-152, 236-242, 240-246, 244-250, 287-293, 309-315,
320-326, 366-372, 423-429, 425-431, 441-447, 503-509, 580-586

FIGURE 65

GGGGACGGGAGCTGAGAGGGCTCCGGGCTAGCTAGGTGTAGGGTGGACGGGCTCCAGGACC
CTGGTGAGGTTCTCTACTTGGCCTCTGGGGGTCAAGACGCAGCACCTACGCCAAAGG
GGAGCAAGCGGGCTGGCCGAGGCCCCAGGACCTCATCTCCCATGTGGAGGAATC
CGACACGTGACGGTCTGTCGGCGTCTCAGACTAGAGGAGCCTGAAACGCCATGGCTCC
AAGAAGCTGCTGCTGGCTTCTGGCTGAGGACCTGAGGAGCCTGAACTGCTGCCCA
GGCAGACACTCGGTGTTGTAAGGGGTCACTGGCTGAGGCTACAGCTGCTGCCCA
CGTTCCGCTATGTGCTGGCAGCTGCACTACTTTCGGTACCGCGGGTCTTGGGCCAC
CGGCTTTGAAGATGCGATGGAGGGCCCTAACGCACATACAGTTTATGTGCCCTGGAACTA
CCAGGACAGCAGCTGGGTCTATAACTTAACTGGAGCGGGACCTCATTGCTTCTGA
ATGAGGAGCTGAGCAGCTGGGTCTGGTCACTGAGACAGGACCTACATCTGTGAGAG
TGGGAGATGGGGTCTCCATCTGGTGTCTCGAAAACCTGAAATTCTATCTAAGAACCTC
AGATCCAGACTCTGGCAGCTGGACTCTGGTCAAGGTCTGGCCAAAGATATATC
CATGGCTTATACAAATGGGGCAACATCATTAGCATTCAGGTGGAAATGAATATGGTAGC
TACAGAGCCTGTGACTTCAGCTACATGAGGACTTGGCTGGCTCTCGTGCAGTCTAGG
AGAAAAAGATCTGCTCTTCACACAGATGGCCCTGAAGGACTCAAGTGTGGCTCCCTCCGG
GACTCTAACCTGAGATTGGGCGACTGACACATGACCAAAATCTTACCCCTGCTT
CGGAAGTATGAAACCCATGGGCAATTGGTAACACTGAGTACTACACAGGCTGGATTAA
CTGGGGCCAGAATCACTCCACACGGTCTGTGTCAGCTGTAACCAAAGGACTAGAGAACATGC
TCAAGTGGGAGCCAGTGTGAAACATGTACATGTGTTCTGGAGGTACCAACTTGGATATTGG
AATGGTGGCAGATAAGAGGGAGCTTCTCGGATTACTACAGCTATGACTATGATGCACC
TATATCTGAAGCAGGGACCCACACCTAACGTTTGTCTCGAGATGTCACTAGCAAGT
TCCAGGAAGTCTGGGACCTTACCTCCCGAGCCCCAAGATGATGCTTGGACCTGTG
ACTCTGCACCTGGGCAATTACTGGCTTCTAGACTGCTTGGCCCGTGGGGCAT
TCATTCAATCTGCAATGACCTTGGCTGAGGCTGTCAGCAGGACCATGGCTCATGGTGTACC
GAACCTATATGACCCATACCAATTGGAGGCAACACCATTGGGTGCAAATAATGGAGTC
CATGACGGTGTCTATGTGATGGTGGATGGGTGTTCCAGGGTGTGTGAGCAGAACATGAG
AGACAAACATTGGAGCGGGAAACTGGGTCACAGGATATCTGGTGGAGAACATGG
GGAGGCTCAGCTTGGCTAACAGCAGTCAAGGGCTGTTGAAGCCACAAATTCTG
GGCCAACAACTCTTACGGTGTGTTCTCTGAAATTGATAACCTTGTGAAGTG
GTGGTTTCCCCTCAGTGGCAAAATGGCATTATCTCAAGCTCTGGCCCCACATTCT
ACTCTAAACATTTCAATTGGCTCAGTTGGGACACATTCTATATCTACCTGGATGG
ACCAAGGGCAAGTGTGGATCAATGGGTTAACTTGGGGCGTACTGGACAAAGCAGGGCC
ACAAACAGACCTCTACGGTCAAGGATTCTGGTGTGTTCTAGGGAGCCTCAACAAATTAA
CATTGCTGGAACTAGAAGATGTACCTCTCAGGCCAACGTCCTAACATTGGATAAGCTATC
CTCAATGCACTAGTACTTGCACAGGACACATATCAATTCCCTTCAGCTGATACACTGAG
TGCTCTGAACCAATGGAGTAAAGTGGGACTGAAAGGTAGGCCGGCATGGTGGCTCATGC
CTGTAATCCCAGCAGTTGGAGGCTGAGACGGGTGGATTACCTGAGGTCAAGGACTTCAAGA
CCAGCCTGGCCAACATGGTCAAAGACCCGCTCCACTAAAAATACAAAATTAGCCGGCGTG
ATGGTGGGCACCTCTAATCCAGCTACTTGGAGGCTGAGGGCAGGAGAATTGCTTGAATCC
AGGAGGAGGAGGTTGCACTGAGTGGAGGTTGTACCTGCACTGCCACTGGCTGACAGTGA
GACACTCCATCTCAAAAAAA

FIGURE 66

MAPKKLSCLRSLLLPLSLTLLPQADTRSFVVDRGHDRFLLDGAPFRYVSGSLHYFRVPRVL
WADRLLKMRWSGLNAIQFYVPWNYHEPQPGVYNFNGSRDLIAFLNEAALANLLVILRPGPYI
CAEWEMGGGLPSWLLRKPEIHLRLTSDPDFLAVIDSWFKVLLPKIYPWLYHNGGNIISIQVE
YGSYRACDFSYMRHLAGLFRALLGEKILLFTTDGPEGLKCGSLRGGLYTTVDFGPADNMTKIF
TLLRKYEPHGPLVNSEYYTGWLWQGQNHSRTSVAVTKGLENMLKLGASVNMYMFHGGTNF
GYWNGADKKGRFLPITTSDYDAPISEAGDPTPKLFLALRDVISKFQEVPGLPLPPPSPKMML
GPVTLHLVGHLLAFLDLLCPRGPIHSILPMTFEAVKQDHGFMLYRTYMTHTIFEPTPFWVPN
NGVHDRAYVMVGDGVFQGVVERNMRDKLFLTGKLGSKLDILVEMGRSLFGSNSSDFKGLLKP
PILGQTILTQWMMFPLKIDNLVKKWWFPLQLPKWPYPQAPSGPTFYSKTFPILGSGVGDFFLYL
PGWTKGQVWINGFNLGRYWTQKQGPQQTLYVPRFLFPRGALNKITLLELEDVPLQPQVQFLD
KPILNSTLHRTHINSLSADTLSASEPMELSGH

2000-05-15-0660

Signal sequence:

amino acids 1-27

N-glycosylation site.

amino acids 97-101, 243-247, 276-280, 486-490, 625-629

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 4-8

Casein kinase II phosphorylation site.

amino acids 148-152, 234-238, 327-331, 423-427, 469-473, 550-554,
603-607, 644-648

Tyrosine kinase phosphorylation site.

amino acids 191-198

N-myristoylation site.

amino acids 131-137, 176-182, 188-194, 203-209, 223-229, 227-233,
231-237, 274-280, 296-300, 307-313, 447-453, 484-490

FIGURE 67

GCTTGAAACACGCTGCAAGCCCCAAGTTGAGCATCTGATTGGTTATGAGGTATTCAGTGCA
ACCCACAATATGGCTTACATGTTAAAAGCTCTCATCAGTACATATCCATTATTTGTGT
TTATGGCTTATCTGCCTACACTCTCTGGTTATTCAGGATACCTTGAAGGAATT
CTTTCGAAAAGTCAGAGAAGAGCAGTTAGTGCACATTCCAGATGTCAAAACGATT
GCGTTCCTCTTCACATGGTAGACAGTATGACCAGCTATATTCCAAGCGTTTGGTGTGTT
CTTGTCAAGTAGTGAAGAAATTAGGGAAATTAGTTGAACCATGAGTGGACATTG
AAAACCTCAGGAGCACATTACACGCCAGGACAAGCAGGAGTTGCATCTGTCATG
CTGTGGGGGTGCCGATGCTCTTGCACAGACCTGGATGTGCTAAAGCTTGAACT
AACTCCAGAAGCTAAAATTCTGCTAAGATTCTCAAATGACTAACCTCAAGAGCTCCACC
TCTGCACTGCCCTGCAAAAGTTGAACAGACTGCTTTAGCTTCTCGCGATCACTTGAGA
TGCCTTCACGTGAAGTTCACTGATGTGGCTGAAATTCTGCTGGGTGTTTGCTCAAAA
CCTTCGAGAGTTGACTTAATAGGCAATTGAACCTCTGAAAACAATAAGATGATAGGACTTG
AACTCTCCGAGAGTTGCCGACCTTAAGATTCTCACGTGAAGAGCAATTGACCAAAGTT
CCCTCCAACATTACAGATGTGGCTCCACATCTAACAAAGTTAGTCATTCTATAATGACGGCAC
TAAACTCTGGTACTGAACAGCCTAAAGAAAATGATGAATGTCGCTGAGCTGAACTCCAGA
ACTGTTGAGCTAGAGAGAACCCACATGCTATTTCAGCCTCTCTAAATTACAGGAACCTGGAT
TTAAAGTCCAATAACATTGCGACAATTGAGGAAATCATCAGTTCCAGCATTAAACGACT
GACTTGTAAAATTATGGCATAACAAAATTGTTACTATTCCCTCCTCTATTACCCATGTCA
AAAACCTGGAGTCACCTTATTCTCTAACACAAAGCTGCAATCCTTACAGTGGCAGTATT
AGTTTACAGAAACTCAGATGCTTAGATGTGAGCTACAAACACATTCAATGATTCCAATAGA
AAATAGGATTGCTTCAGAACCTGCACTTGATATCAGCTGGGAAACAAAGTGGACATTCTGC
CAAACAAATTGTTAAATGCTAAAGATTGAGGACTTTGAATCTGGACAGAACTGCACTCACC
TCACCTCCAGAGAAAGTTGGTCAGCTCTCCAGCTACACTGAGCTGGAGCTGAAGGGAACTG
CTTGGACCGCTGCCAGCCAGCTGGGCACTGTCGGATGCTCAAGAAAAGCGGGCTGTTG
TGGAGATCACCTTTGATACCCGCCACTCGAAGTCAAAGAGGCATTGAATCAAGACATA
AAATATTCCCTTGCAAATGGGATTAAACTAAGATAATATGACAGTGATGTGCAAGGAAAC
AACTTCCTAGATTGCAAGTGTCACTGACAGTTATTACAAGATAATGCATTAGGAGTAG
ATACATCTTTAAATAAAACAGAGAGGATGCATAGAAGGCTGATAGAAGACATAACTGAAT
GTTCAATGTTGTTAGGGTTAAGTCATTCAATTCCAAATCATTTTTTTTCTTTGGGG
AAAGGGAAAGAAAAATTATAACTAATCTGGTTCTTTAAATTGTTGTAACCTGGAT
GCTGCCGCTACTGAATGTTACAAATTGCTTGCCTGCTAAAGTAAATGATTAAATTGACATT
TTCTTACTAAAAAAAAAAAAAA

FIGURE 68

MAYMLKKLLISYISIICVYGFICLYTLFWLFRIPLKEYSFEKVREESSFSDIPDVKNDAFL
LHMVDQYDQLYSKRGFVFLSEVSENKLREISLNHEWTFEKLRQHISRNAQDKQELHLFMLSG
VPDAVFDLTDLVLKLELIPAKIPIAKISQMTNLQELHLCHCPAKVEQTAFSFLRDHLRCLH
VKPTDVAEIPAWVYLLKNLRELYLIGNLNSENNKMIGLESLRELRHLKILHVKSNLTKVPSN
ITDVAPEHLTKLVIHNDGKLLVLNLSLKKMMNVAELELQNCELERIPHAIFSLSNLQELDLKS
NNIRTIEEIISFQHLKRLLTCLKLWHNKIVTIIPPSITHVKNLESLYFSNNKLESLPVAVFSLQ
KLRCLDVSYNNISMIPIEGGLLQNLQHLHITGNKVDILPKQLFKCIKLRTLNLGQNCITSPL
EKVGQIQLSQLTQLELKGNCLDRLPAQLGQCRMLKKSGLVVEDHLFDTLPLEVKEALNQDINIP
FANGI

Signal sequence:

amino acids 1-20

N-glycosylation site.

amino acids 241-245, 248-252, 383-387

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 326-330

Casein kinase II phosphorylation site.

amino acids 48-52, 133-137, 226-230, 315-319, 432-436, 444-448

Tyrosine kinase phosphorylation site.

amino acids 349-355, 375-381

N-myristoylation site.

amino acids 78-84, 124-130, 212-218, 392-398

FIGURE 69

CCACGCGTCCGGCCTTCTCTGACTTGCATTTCATTCTTCTGACAAACTGACTTTTTTATTCT
TTTTTCCATCTGGCCAGCTGGGATCTAGGGCCCTGGAAAGACATTGTTTACACATAAGGAT
CTGTGTTGGGTTCTCTTCCCTCCCTGACATTGGCATTGCCTAGTGGTGTGTTGGGGAGGACACGCTGG
GCTCAGTGCCTGCTTGGCAGCTTATCTCCCTGAGTACATCGAACAGCTTGTGCTGAGTACAGTGGCTGTC
ATCGCTGGGTATCTCGCCGGCTGCTCTGCTGAGTATGTTCTGCTGCTGTTACAAATACACAC
GGCTAAAGCTGCAAGGAACTGAAGCTGTGGCTGTAAGAAATACACACCCAGACAAGGTGTGGGGCCCAAG
AACAGCCAGGCAAAACATTGCAACGGAGTCTGTGTCCTGGCAGATGGCTGAGGAGTATAGAATGTGTC
AGTTTGATTCCTGCACTTGTGTCAGGACATAATAGGGGCTCTGAGTTAGGAAAGGCTCCCTTCTCAA
GCAGAGCCCTGAAAGACTTCAATGATGCAATGAGCTCTGGTGTGCAAGGACAGAGAAAGGCCACAG
CTCCCATCAGTTTATGGAAAATAACTCAGTGGCTGCTGGGAAACGGCTGCTGGAGATCCCTACAGAGACITC
CACTGGGGCAACCCCTTCAGGAAGGAGTGGGGAGAGAACCTCAGTGTGGGAATGCTGATAAACAGCTCA
CACAGCTGCTTATTCTCAACAAATCTACCCCTTCGGTGGCAACTGACCTTCCCTGGAGGTGTCAGAAA
GCTGATGTAACACAGAGCTATAAAAGCTGTCGCTTIAAGGCTGCCAGCGCCATTGCCAAAATGGAGCTGTA
AGAAGGCTCATGCCCATTGACCTTCTTAATTTCTCTGTGTCAGGAGCTGACAATGGGGAGGCTGAAGGCAAT
GCAGAGCTGCAACAGTCAGTGTGGGGTGCCTAATGGCCAGAGCCAAACAGGCAATGATCTGCACAACTCAATCC
AGTGAAGACTGCACTGGGGCAACCCCTGAGGAAACAGGAAACAAAGCTCAAGAATTATCTTCTATGTCAGCTT
GATCCAGATGGAGACTGTGAAACATTAAGAACTTGTGTTCTGACGGAACTTCCAGCAATGGGGCTCTGCTAGGG
CAAGCTGCACTGAAACAAAGCAACTGTTCTGTTATGTAACATCAGCTGAACTTCAATGGGGTTCAGTGT
GACTCAGCAGAACTTCAAGAACTCTTGTCTCTACTACTCTCTCCCTAACATCTTATTCCAAACTG
GCGGGTTACTGGATACCTTGGAAAGGATCTTCAACAGGCCCAATTACCCAAAGGCCATCTGAGCTGCTTAT
TGTGTTGGCCTACATCAAGCTGGAAAGGATACAGGAAACAAACTTCAAGGATTTCTCTGAAATAGAC
AAACATGTCCTTCTGATGTCCTTCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG
GGCGGGTGTGACTCCACCTGGAAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG
TTTGAAAAGACTTACTCTGAAATCACCATATTAGTGGAAATGGGACATACTTCAAGTGGAGATAATAACATCAACA
TACCTGGGGGATTCTCTCTCACACCTCAATTAATGCAACTTCAACACTACATCTTAACTCTGCTTCT
GACAGGATGAGGATTTATAACAAATCTTACCTAACAGGCTTTAACCTCTAACATGGGAAATAACTTGAACAA
GACCCAACTGCAACCCAAATATCAAATGTTGTGGAAATTCTCTCTCTTCAATGGAATGGTACAACTGAG
AAAGTAGAGAATGTCATTAATCTTCAACCAAAATATACTCCTTCTCTGCTCATCTCAACTCTGAAAGTGT
CTGCAAGGAACTCCAGATGGGCAAAATATAACCCAGCATGGCTCTTGTGAATCCAACTTCA
GAAGATGATGTAATCAAAGTCAAATGCACTGGGCAAAATATAACCCAGCATGGCTCTTGTGAATCCAACTTCA
TTTGAAAAGACTTACTCTGAAATCACCATATTAGTGGAAATGGGACATACTTCAAGTGGAGATAATAACATCAACA
ACCTCAGATCCAAATTGGTGGTGTCTGTGATACCTGTAAGGCTCTCCACCTCTGACTTGTGCTCATCTCAACC
TACGACCTAATCAGAGTGGATGAGTGTGAGATGAAACTTGTAAAGGGTGTACCTTGTGACACTATGGGAGA
TTCAGTTAACTGCTTAAATCTTGTGAAAGTGTGAGCTGTGTTCTGAGTGTAAAGTTGTGATGATG
ACCGATGACCAACAGCTCTGCTCACTCAAGGTGTGTTCTCCAGAACACAGAGACATTCTCATATAATG
AAAACAGATTCCTACATAGGACCCATTGCTGAAAGGGGATGCAAGTGGCAATTCAAGGATTTCTGCT
GAACACATGCGGAAGAAACTCAAACAGGCTTCAACAGTGTGCACTGTTTCTTCTCATGGGTTCTAGGCTG
ATGTGGTGAATGTGAGGCAACTCACAGTGTGAGGCAATTGTGAATACACGGGAGACTACAAATACAGAAGCTG
CAGAACTTAACTAACAGGTCACCCACTAAGTGTGAGACATGTTCTCAGGATGCAAAGGAAATGCTACCTCGT
GCCTACACATATTATGAATAATGAGGAAGGGCTGAAAGTGTGACACACAGGCTGATGTTAAAAAA

FIGURE 70

MELVRRLLMPLTLLILSCLAEELTMAEAEGNASCTVSLGGANMAETHKAMILQLNPSENCTWTI
ERPENKSIRIIIFSYVQLDPDGSCESENIKVFDGTTSNGLGQVCSKNDYVPVFESSSSTLT
FQIVTDSARIQRTVFVFFYFFSPNISIPNCGGYLDTLEGSFTSPNPKPHPELAYCWHIQV
EKDYKIKLNFKEIFLEIDKQCKFDLAIYDGPSTNSGLIGQVCGRVTPTFESSSNSLTVVLS
TDYANSYRGFSASYTSIYAENINTTSLTCSSEDRMRVIIISKSYLEAFNSNGNNLQLKDPTCRP
KLSNVVEFSVPVLNGCGTIRKVEDQSITYTNIIITFSASSTSEVITRQKQLQIIVKCEMGNST
VEIIYITEDDVIIQSQNALKYNTSMALFESNSFEKTIILESPYYVDLNQTLFVQVSLHTSDPN
LUVVFLDTCRASPTSDFASPTYDLIKSGCSRDETCKVYPLFGHYGRFQFNNAFKFLRSMSSVYL
QCKVLLICDSSDHQSRCNQGCVSRSKRDISSYYWKWKTDSIIGPIRLKRDRSASGNSGFQHETHA
EETPNQPFNSVHLFSFMVLALNVTVTATITVRHFVNQRADYKYQKLQNY

Signal sequence:

amino acids 1-24

Transmembrane domain:

amino acids 571-586

N-glycosylation site.

amino acids 29-33, 57-61, 67-71, 148-152, 271-275, 370-374,
394-398, 419-423

Casein kinase II phosphorylation site.

amino acids 22-26, 108-112, 289-293, 348-352, 371-375, 379-383,
408-412, 463-467, 520-524, 556-560

Tyrosine kinase phosphorylation site.

amino acids 172-180, 407-415, 407-416, 519-528

N-myristoylation site.

amino acids 28-34, 38-44, 83-89, 95-101, 104-110, 226-232

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 7-18

FIGURE 71

GGCGGAAGAACAGCGCTCCCGAGGCCGGGGAGCCTGCAAGAGGGACAGCCGGCTGCGCCG
GGACATGCGGCCGCCAGGAGCTCCCAGGCTCGCTTCCCGTGTGCTGTTGCTGCTG
TGCCTGCGCCGCCGCGTGCCTGCCACAGGCCACCGCCTGCACCCACCTGGGAGTCC
CTGGACGCCGCCAGCTGCCCGCTGGTTGACCAGGCCAGTTCGGCATCTTCATCCACTG
GGGAGTGTTCCTGCCAGCTTCGGTACCGAGTGGTTCTGTTGCTGTTGAGTATGGCAAAAGGAAA
AGATACCGAAGTATGTGGAATTATGAAAGATAATTACCTCCCTAGTTCAAATATGAAGAT
TTTGGACCACTATTACAGCAAATTTTAATGCCAACAGTGGCAGATATTTCAGGC
CTCTGGTGCCTAAATACATTGCTTAACCTTAAACATCATGAAGGCTTACCTTGTGGGGT
CAGAATATTCTGTTGAACTGGATGCCATAGATGGGGCCAAGAGGGGACATTGTCAAGGAA
CTTGAGGTAGCCATTAGAACAGTACCTGCGCTTGGACTGTACTATTCCCTTTGA
ATGGTTTCATCCGCTTCTGAGGATGAATCCAGTTCATTCCATAAGCGGAATTCCAG
TTTCTAAGACATTGCCAGAGCTTCTAGTGGTACTGAAACACTATCAGGCTTGTTG
TCGGTGGTACGGGAGCAGGGGACACGGGATCAACTGAGAACAGCACGGCTTCTGGCTGGT
ATAATAATGAAAGCCCACTTCCGGGACAGTAGTCACCAATGATGTTGGGGAGCTGGTAGCA
TCTGTAAGCATGGTGGCTCTATACCTGCAAGTGTGTTATAACCCAGGACATTTGGCA
AATCTCTGACTATCTTAACTTGAAGAAATTGGTGAAGCAACTTGTAGAGACAGTTTGTG
GAGGAAATCTTTGATGAATATTGGGCCACACTAGATGGCACCATTCTGTAGTTTGTG
GAGCAGTGGCAAGTGGGTCTGGCTAAAGTCAATGGAGAAAGCTATTATGAAACCTA
TACCTGGCATTCCAGAATGACACTGTCAACCCAGATGTGGTACACATCCAACGCTAAAG
AAAAATTAGTCATGCCATTCTTAAATGGCCACATCAGGACAGTGTCTTGGCCAT
CCAAAGCTATTCTGGGGCAACAGAGGTGAAACTACTGGCCATGGCACAGCCACTTAAC
GATTTCTTGGAGCAAATGGCATTATGGTGAAGACTGCCACAGCTAACATTCTCATG
CGTGTAAATGGGCTGGCTTAACCTAAATGTGATCTAAAGTGCAGCAGTGGCTG
ATGCTGCAAGTTATGTCTAAGGCTAGGAACATCAGGTTGTCTATAATTGTAGCACATGGAGA
AAGCAATGAAACTGGATAAAAGGAAATTATTGGCAGTTCAAGCTTCTTCCACTA
AATTTCCTTAAATTACCCATGTAACCATTTAACCTCTCAGTGCACCTTGCCATTAAAGTC
TCTTCACATTGATTGTTCTCATGTGACTCAGAGGTGAGAATTTCACATTATAGTAG
CAAGGAATTGGTGGTATTATGGACCGAACTGAAAATTATGTTGAAGCCATATCCCCATG
ATTATATAGTTATGCACTTAATATGGGGATATTCTGGGAAATGCATTGCTAGTCAAT
TTTTTTCTGTGCCAACATCATAGAGTGTATTACAAATCTAGATGCCATAGCTACTACA
CACCTAATGTGTATGGTATAGACTGTTGCCCTAGGCTACAGACATATAACAGCATGTTACTG
AATACTGTAGGCAATAGTAACAGTGGTATTGTGAACTATGGAAACATATGGAAACATAGAGAAG
GTACAGTAAAATACTGTAAAATATGGCAGCTGTATAGGGCACTTACCCAGAATGGAG
CTTACAGGACTGCAAGTGTCTGGGTGAGTCAGTGAGTGAATGTGAAGGCTAGGACATTA
TTGAACACTGCCAGACGTATAAAACTGTATGTTAGGCTACACTACATTATGAAAC
GTTTTCTTCTTCAATTAAACATAAGTGTACTGTAAACTTACAACGTTTAAATT
TTTAAACCTTTGGCTTTGTAAACACTTAGCTTAAACATAACACTCATTGTGCAA
ATGTAA

FIGURE 72

MRPQELPRLAFLPLLLLLLPPPPCPAHSATRFDPTWESLDARQLPAWFDQAKFGIFIHWG
VFSVPSFGSEWWYQKEKIPKYVEFMKDNYPPSFKYEDFGPLFTAKFFNANQWADIFQAS
GAKYIVLTSKHHEGFTLWGSEYSWNWNAIDEGPKRDIVKELEVAIRNRTDLRGFLYYSLFEW
FHPLFLEDESSSFHKRQFPVSKTLPELYELVNNYQPEVLWSDGDGGAPDQYWNSTGFLAWLY
NESPVVRTVVTNDRWGAGSICKHGGFYTCSDRYNPGHLLPHKWENCMTIDKLSWGYRREAGI
SDYLTIEELVKQLVETVSCGGNLLMNIGPTLDGTISVVVFEEQLRQVGWSWLKVNGEAIYETY
WRSQNDTVTPDWYTSKPKEKLVYAIFLKWPMSGQLFLGHPKAILGATEVKLLGHGQPLNWI
SLEQNGIMVELPQLTIHQMPCKWGWLALTNVI

TOOTZ = STS200600

Signal sequence:

amino acids 1-28

N-glycosylation site.

amino acids 171-175, 239-243, 377-381

Casein kinase II phosphorylation site.

amino acids 32-36, 182-186, 209-213, 227-231, 276-280, 315-319,
375-375

Tyrosine kinase phosphorylation site.

amino acids 361-369, 389-397

N-myristoylation site.

amino acids 143-149, 178-184, 255-261, 272-278, 428-434

Leucine zipper pattern.

amino acids 410-432

Alpha-L-fucosidase putative active site.

amino acids 283-295

FIGURE 73

AGCAGGGAAATCCGGATGTCTCGGTTATGAAGTGGAGCAGTGAGTGTGAGCCTCAACATAGT
TCCAGAACCTCTCATCCGGACTAGTTATTGAGCATCTGCCTCATATCACCGAGGCCATC
TGAGGTGTTCCCTGGCTCTGAAGGGTAGGCACGATGGCCAGGTGCTTCAGCCTGGTGTG
CTTCTCACTTCCATCTGGACCACGAGGCTCTGGTCAAGGCTCTTGCGTGAGAAGAGCT
TCCATCCAGGTCTCATGGAGAATTATGGGATCACCCCTTGAGCAGAAAGGCCAACCGC
AGCTGAATTTCACAGAAGCTAAGGAGGCTGTAGGCTGTGGACTAAGTTGGCCGGAAG
GACCAAGTGAACAGCCTGAAAGCTAGCTTGAAACTTGAGCTATGGCTGGGTTGGAGA
TGGATTCTGGTCTATCTCTAGGATTAGCCCCAACCCCAAGGTGAGCTGGGAAAATGGGTTGGGTG
TCCTGATTGGAAAGGTTCCAGTGAGCCGAGCTTGAGCCTATTGTTACAACACTCATCTGAT
ACTTGACTAACTCTGTGATTCCAGAAGATTACCAACCAAGATCCATATTCAACACTCA
AACTGCAACACAAACAGAATTATTGTCACTGAGCTACCTACTCCGGTGGCATCCCCCT
ACTCTACAATACCTGGCCCTACTACTCTCTCTGCTCAGCTTCCACCTCTCACCG
AGAAAAAAATTGATTGTGTCACAGAAGATTATGGAAACTAGCACCATGTCTACAGAAC
TGAACCCATTGTTGAAAATAAGCAGCATTAAGAATGAAGCTGCTGGGTTGGAGGTGTC
CCACGGCTCTGTAGTGTCTCTCTCTCTTGTGCTGAGCTGCTGGATTGATTGATTG
TATGTCAAAAGGTATGTGAAGGCCCTCCCTTAAACAAAGAATCAGCAGAAGGAATGAT
CGAACCCAAAAGTGTAAAGGGAGAACGCCAATGAGCAACCCATAAGGAAATCAAAGA
AAACTGATAAAACCCAGAAGAGTCCAAGAGTCCAAGCAGAAACTACCGTGCAGTCCTGAA
GCTGAAGTTAGATGAGACAGAATGAGGAGACACCTGAGGCTGGTTCTTCTGCTCC
TTACCCCTGCCAACGGGAAATCAAAGGCCAACAGAAGAACCAAAGAAGAACGGCT
GGTCTTAACTGGAAATCAGCTAGGACTGCCATTGGACTATGGAGTGACCAAAGAGAAC
CCTTCCTTATTGTAAACCTGTCTGGATCTTATCTCTACCTCCAAAGCTTCCACGCC
TTTCTGCTGCTATGCTCTATAATATCCCACGGGAAAGGAGTTTGCAAAAGTCAA
GGACCTTAAACATCTCATGATTCAGTGTGAAAAGGGCTCTGGCTGAGGCTAGG
TGGGTGAAAGCCAAGGAGTCACTGAGACCAAGGCTTCTCTACTGATTCGAGCTCAGAC
CCCTTCTTCAGCTCTGATCCACCTGACATGCTTCTGAGGCCGGTA
AGAGCAAAAGAATGGCAGAAAAGTTAGCCCCGTGAAAGCAGTGGAGATTCTCATAACTTGAG
ACCTAATCTGTAAAGCTAAAAGAACATAGAACAAAGGCTGAGGATACGACAGTACACT
GTCAGCAGGGACTGTAAACACAGACAGGGTCAAAGTGTGTTCTGAAACACATTGAGTTGGA
ATCACTGTTAGAACACACACACTTTCTGGTCTTACCACTGCTGATATTCTCT
AGGAAATATACTTTACAAGTAACAAAATAAAAACCTCTTATAAATTCTATTCTATCTGA
GTTACAGAAAATGATTACTAAGGAAGGATTACTCAGTAATTGTTAAAAGTAATAAAATTCA
ACAAACATTGCTGAATAGCTACTATATGTCAGTGCTGCAAGGTATTACACTCTGTAAT
TGAATATTATTCTCAAAAATTCAGCATGATAGAACCGCTATCTGGAGGCTATTCT
GTTTGATATTCTAGCTTACTCTCAACTAATTCTATTCTGAGACTAATCT
ATTCATTCTCTAATATGGCAACCATTATAACCTTAATTATTAAACATACCTAAGAAC
TACACATTGTTACCTCTATACCAAAAGCACATTAAAAGTGCCTTAACAAATGTTAC
GCCCTCCCTTCAACAAGAAGGGACTGAGAGATGCAGAAATATTGTGACAAAAAATTAA
AGCATTAGAAAACCTT

FIGURE 74

MARCFSLVLLTSIWTRLLVQGSLRAEELSIQVSCRIMGITLVSKKANQQLNFTAKEACR
LLGLSLAGKDQVETALKASFETCSYGVGDGFVVISRISPNNPKCGKNGVGLIWKVPSRQF
AAACYNSSDTWNSCIPEIITTKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIAPPTTPP
APASTSIPRRKKLICVTEVFMETSTMSTETEPFVENKAASKNEAAGFGGVPTALLVIALLFF
GAAAGLGFCYVKRYVKAFFPTNKNQQKEMIETKVVKEEKANDSNPNEESKKTDKNPEESKSP
SKTTVRCLEAEV

Signal sequence:

amino acids 1-16

Transmembrane domain:

amino acids 235-254

N-glycosylation site.

amino acids 53-57, 130-134, 289-293

Casein kinase II phosphorylation site.

amino acids 145-149, 214-218

Tyrosine kinase phosphorylation site.

amino acids 79-88

N-myristoylation site.

amino acids 23-29, 65-71, 234-240, 235-239, 249-255, 253-259

1000-990-980-970-960-950-940-930-920-910

FIGURE 75

AGATGGCGGCTTGGCACCTAATTGCTCGTATTGGTCCGCGACTTCACGATGGCTCGCCCCACCTTACTACCTCTGTCGCCCTGCTCTGCTGCCCTACTCGTAGGAAACTGCCGCCGCTCTGCCACGGTCTGCCACCCAAACGCGAAGACGTTACCCGTGTGACTTTGACTGGAGAGAAGTGGAGATCTGATGTTCTCAGTGGCATTGTGATGATGAAGAACCGCAGATCCATCACTGAGAACATATAGGCAACATTTCATGTTAGTAAAGTGGCAACACAATTCTTTCTCCGCTTGGATATTGCATGGGCTACTTACATCACACTGCACTGTTCTGATGACGTGCAAACCCCCCTATATATGGGCCCTGAGTATATCAAGTACTTCATGATAAAACCATTGATGAGGAACTAGAACGGGACAAGAGGGTCATTGGATTGGAGTTCTTGCAAATTGGTCTAATGACTGCCAATCATTGCCCTATCTATGCTGACCTCTCCCTAAATACAACTGTACAGGGCTAAATTGGAGGTGGATGTTGGACGCTATACTGATGTTAGTACCGGGTACAAAGTGAGCACATCACCCTCACCAAGCAACTCCCTACCCCTGATCTGTTCAAGGGCGAACGGAGCAATGGCGGGCCACAGATTGCAAGAAAGGACGGCTGTCATGGACCTTCTCTGAGGAGAATGTGATCGAGAAATTAACTTAAATGAGCTATAACCAGGGCCAAGAAACTATCAAGGCTGGAGACAATATCCCTGAGGAGCAGGCTGTGGCTCAACCCCCACACAGTGTCAATTGGGGAAAACAAGAAGGATAAAATAGATCTCACTTTGGCAGTGTCTCTCTGTCAATTCCAGGCTTTCCATAACCCAAGCCTGAGGCTGCGAGCTTNTATTNATGTTTCCCTTGCTGNGACTGGNTGGGGCAGCATGCGAGCTCTGATTAAAGAGGCATCTAGGGAATTGTCAGGCACCCCTACAGGAAGGCTGCCATGCTGTGGCCAAGTGTTCACTGGAGCAAGAAAGAGATCTCATAGGACGGAGGGGAAATGGTTCTCCCTCAAGCTGGCTCAGTGTGTTAACTGCTTATCAGCTTACAGACATCTCCATGGTTCTCCATGAAACTCTGTTGTTACATCTCCCTCTAGTTGACCTGCAACAGCTGGTAGACCTAGATTAAACCTAAGGTAAGATGCTGGGGTATAGAACGCTAAGAATTTCACCCAAAGGACTCTGCTTCTTAAGCCCTCTGGCTTGTGTTATGGCTTCATTAAAGTATAAGCTAACCTTGTGCGTAGCTAACAGGAGAACCTTAAACCAAAAGTTTTATCATTGAGACAAATTGAAACAACCCCCCTATTGTGGGGATTGAGAAGGGTGAATAGAGGCTTGGAGACTTCTCTTGTGTTGAGACTGGAGGAGAAATCCCTGGACTTTCACTAACCCCTGACATACTCCCCACACCCAGTTGATGGCTTCTGTAATAAAAAGATTGGATTCTCTTTG

FIGURE 76

MAVLAPLIALVYSPVRLSRWLAQPYYLLSALLSAAFLVRKLPPLCCHGLPTQREDGNPCDFD
WREVEILMFLSAIVMMKNRRSITVEQHIGNIFMFSKVANTILFFRLDIRMGLLYITLCIVFL
MTCKPPLYMGPEYIKYFNDKTIDEELERDKRVTWIVEFFANWSNDQCQSFAPIYADLSLKYNC
TGLNFGKVDVGRYTDVSTRYKVSTSPLTKQLPTLILFQGGKEAMRRPQIDKKGRAVSWTFSE
ENVIREFNLNELYQRAKKLSKAGDNIPEEQPVASTPTTVSDGENKKDK

Signal sequence:

amino acids 1-48

Transmembrane domain:

amino acids 111-125

N-glycosylation site.

amino acids 165-169, 185-189

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 154-158, 265-269

Casein kinase II phosphorylation site.

amino acids 51-55, 145-149, 245-249, 286-290, 288-292

N-myristoylation site.

amino acids 188-194, 225-231

Myb DNA-binding domain repeat signature 1.

amino acids 244-253

FIGURE 77

GGACAGCTCGGGCCCCGAGAGCTAGCCGTCGAGGAGCTGCCTGGGACGTTGCCCTG
GGCCCCCAGCCTGGCCGGGTCACCCGGCATGAGGAGATGGCCTGTTGCTCTGGTCCCA
TTGCTCCTGCTGCCGGCTCTACGGACTGCCCTCTACAAACGGCTTACTACTCCAACAG
CGCCAACGACCAGAACCTAGGCAACGGTCACTGGCAAAGACCTCTTAATGGAGTGAAGCTGG
TGGTGGAGACACCCGAGGAGACCCGTTCACTTACCAAGGGGCCAGTGTGATCCTGCCCTGC
CGCTACCGCTACGAGCCGGCCCTGGTCTCCCGCGGCGTGTGCGTGTCAAATGGTGAAGCT
GTGCGAGAACGGGCCCCAGAGAACGGACGTGCTGGTGGCATCGGGCTGAGGCACCGCTCT
TTGGGGACTACCAAGGCCGCGTCACCTGCGGAGGACAAAGAGCATGACGTCTCGCTGGAG
ATCCAGGATCTGCGCTGGAGGACTATGGCGTTACCGCTGTGAGGTATTGACGGCTGGA
GGATGAAAGCGGTCTGGTGGAGCTGCGGGGTGTGGCTTTCTTACAGTCCCCA
ACGGGCGCTACAGTCACCTCCACGAGGGCCAGCAGGTCTGTGAGGAGCAGGCTGCCGTG
GTGGCCTCCTTGTAGCAGCTTCCGGGCTGGGAGGGAGGGCCTGGACTGGTCAACCGCGG
CTGGCTGCAGGATGCTACGGTGCAGTACCCCATCATGTTGCCCCGGCAGCCCTGCCGTGGCC
CAGGCCCTGGCACCTGGCGTGCAGAACGCTACGGCCCCGCCACCGCCGCTGCACCGTATGAT
GTATTCTGCTTCGCTACTGCCCTCAAGGGCGGGTGTACTACCTGGAGCACCTGAGAACGCT
GACGCTGACAGAGGAAGGGAGGCTGCCAGGAAGATGATGCCACGATGCCAAGGGGGAC
AGCTTTGCCCTGGAAGTCCATGGCTGGACCGCTGCGACGCTGGCTGGCTGGCAGAT
GGCAGCGTCCGCTACCCCTGTGGTTCACCCGATCCTAACGTGGGGCCCCAGAGCCTGGGT
CCGAAGCTTGCTCCCCGACCCGAGAGCCGCTGTGACGGTTACTGCTACCGCCAGC
ACTAGGACCTGGGGCCCTCCCTGCCGATCCCTCACTGGCTGTGTATTATTGAGTGGTT
CGTTTCCCTTGTGGGTTGGACCATTTAACTGTTTATACCTCTCAATTAAATTCT
TTAACACATTTTTACTATTTTGTAAAGCAAACAGAACCCATGCCCTCCCTGCTCTG
GATGCCCACTCCAGGAATCATGCTTGCTCCCTGGGCATTGCGGTTTGTGGCTCTG
GAGGGTCCCCGCATCCAGGTGGCTCCCTCCCTAACGGAGGGTGGTGGCCAGAGTGGC
GGTGGCCTGTCTAGAATGCCGGGGAGTCGGGAGCTGGGGCACAGTCTCCCTGCC
CAGCCCTGGGGAAAGAACGGGCTCGGGGCCCTCGGAGCTGGCTTGGGCCCTCTCTGCC
CACCTCTACTTCTGTGAGGCCGCTGACCCAGTCTGCCACTGAGGGCTAGGGCTGGAA
GCCAGTTCTAGGCTTCCAGGCAGAACATCTGAGGGAGGAAGAAACTCCCCCCCCGTTCCCT
TCCCTCTCGGTTCCAAAGAATCTGTTGTGTCATTGTTCTCTGTTCCCTGTGTGG
GGAGGGGCCCTCAGGTGTGTACTTTGGACAATAATGGTGTATGACTGCCCTCCGCCAA
AA
AA

FIGURE 78

MGLLLLVPLLLLPGSYGLPFYNGFYYNSNSANDQNLGNHGKDLLNGVKLVVETPEETLFTYQ
GASVILPCRYRYEPALVSPRRVRVKWWKLSENGAPEKDVLVAIGLRHRSFGDYQGRVHLRQD
KEHDVSLEIQDRLLEDYGRYRCEVIDGLEDESGLVELELRGVVFYQSPNGRYQFNFHEGQQ
VCAEQAAVVASFEQLFRAWEEGLDWCNAGWLQDATVQYPIMLPRQPCGGPGLAPGVRSYGPR
HRRLHRYDVFCFATALKGRVYYLEHPEKLTLTEAREACQEDDATIAKVGQLFAAWKFHGLDR
CDAGWLADGSVRYPVVPHPMCGPPEPGVRSGFPDPQSRLYGVYCYRQH

Signal sequence:

amino acids 1-17

Casein kinase II phosphorylation site.

amino acids 29-33, 53-57, 111-115, 278-282

Tyrosine kinase phosphorylation site.

amino acids 137-145

N-myristoylation site.

amino acids 36-42, 184-190, 208-214, 237-243, 297-303, 307-313

100902615 - 074001

FIGURE 79

GGAGAGCGGAGCGAAGCTGGATAACAGGGGACCGGATGATTGGCGACCATCAGTTCTGCTGC
TTCTGTTGCTACTGAGGCACGGGGCCAGGGGAAGCCATCCCAGCAGCCAGGGCTCATGGC
CAGGGGAGGGTGCACCAGCGCCCCCTGAGCGACGCTCCCCATGATGACGCCACGGGAA
CTTCCAGTAGCACCAGGGCTTCTGGGACGGGAAGTGGCAAGGAATTGACCAACTCA
CCCCAGAGGAAGCCAGGCCGCTCTGGGGCGATCGTGACCGCATGGACCGCGGGGGAC
GGCGACGGCTGGGTGTCGCTGGCGAGCTCGCGCTGGATCGCGCACACGCGAGCGGA
CATACGGGACTCGGTGAGCGGGCTGGGACACGTACGACACGGGACCCGACGGGTGTGG
GTTGGGAGGGAGCTGCGCAACGCCACCTATGGGCACTACGGGCCGGTGAAGAATTGAC
GTGGAGGATGCAGAGACCTACAAAAAGATGCTGGCTGGGACGAGCGGCTTCCGGTGGC
CGACCAAGGATGGGACTCGATGGCCACTCGAGAGGGAGCTGACAGCCTCTGACCCCGAGG
AGTTCCCTCACATGCGGACATCGTATTGCTGAAACCTGGAGGACCTGGACAGAAACAAA
GATGGCTATGTCAGGTGGAGGAGTACATCGGGATCTGTACTCAGCCGAGCCTGGGAGGA
GGAGCCGGCTGGGTGAGACGGAGGGAGCGAGCTTCCGGACTTCCGGATCTGAAACAAGG
ATGGGCACCTGGATGGGAGTGAGGTGGGCACTGGGTGCTGCCCTGCCAGGACCAGCC
CTGGTGGAAAGCCAACACCTGCTGACAGAGAGCGACACGGACAAGGATGGGCGCTGAGCAA
AGCGGAAATCTGGTAATTGGAACATGTTGTGGGAGCTCAGGCCACCAACTATGGCGAGG
ACCTGACCCGGCACACGATGAGCTGTGAGCACCGCGCACCTGCCACAGCCTCAGAGGCCG
CACAAATGACCGGAGGGGGCCCTGTTCTGGCCCTCCCTGTCCAGGCCCCGAGGAG
GCAGATGCACTCCAGGCATCTCTGCCCTGGGCTCTCAGGGACCCCTGGGTGCGCTTC
TGTCCCTGTCAACCCCCAACCCAGGGAGGGGCTGTGATAGTCCAGAGGATAAGCAATAC
CTATTCTGACTGAGTCTCCAGCCCAGACCCAGGGACCCCTTGGCCCAAGCTCAGCTCTAA
GAACCGCCCCAACCCCTCCAGCTCAAATGAGCCTCCACACATAGACTGAAACTCCCT
GGCCCCAGCCCTCTCTGGCTGGCCTGGGACACCTCCCTCTGCCAGGAGGCAATAA
AAGCCAGCGCCGGGACCTTGGAAAAA
AAAAAAAAAAAAAA

FIGURE 80

MMWRSPSLLLLLLLRLHGAQGKPSDAGPHGQGRVHQAAPLSDAPHDDAHGNFQYDHEAFLGR
EVAKEFDQLTPPEESQARLGRIVDRMDRAQDGDGVWSLAEHLRWAIAHTQQRHIRDVSAAWDT
YDTRDGRGVWEELRNATTYGHYAPGEEFHVDEDAETYKKMLARDERRFRVADQDGDSMATE
ELTAFLHPEEFPHMRDIVERIAETLEDLDRNKGDVQVEEYIADLYSAEPGEEEPAWVTERQQ
FRDFRDLNKDGHLGSEVGHWVLPPAQDQPLVEANHLLHESDTDKDGRLSKAEILGNWNMFV
GSOATNYGEDLTHHDEL

Signal sequence:

amino acids 1-20

N-glycosylation site.

amino acids 140-144

Casein kinase II phosphorylation site

amino acids 72-76, 98-102, 127-131, 184-188, 208-212, 289-293, 291-295, 298-302

N-myristoylation site

amino acids 263-269 311-317

Endoplasmic reticulum targeting sequence

amino acids 325-330

FIGURE 81

GGGGCCTTGCCTTCCGACTCGGGCGCAGGGGGATCTCGAGCAGGTGCGGAGCCCCGG
GCGGGCGGGCGGGTGCAGGGGATCCCTGACGCCCTCTGCCCTGGTACACCGATCTCG
CTGCTCTGCTCGCTTGGCCCGGAGGCGCTCCAGACCTAGAGGGGCGCTGGCCTGGAGCAG
GGCTTCGCTCGATTTGCCGCGAGGCGCTCCAGACCTAGAGGGGCGCTGGCCTGGAGCAG
CGGGGCTGCTGCTGCTCTCCCTCTGCCGACCCCTGGCCTTGCCTCGCCGATTCTCCCTCTCCAG
GAGGAGGTGACCGCGGGGGCTCCCGCAGGGGGGGGGGGATCCGAAGGGTGCAGGGCTCT
GTGTGAGCAGCTATCAGTCACC**ATGTC**CCGAGCGATCCCGCTCTGGCCTCGGCTCGGTG
TGTCTGCTGCTGCTGCCGGGGCCGCGGGCAGCGAGGGAGCGCTCCATTGCTATCACATG
TTTACAGGGGCTGGACATCAGGAAAGAGAACGAGATGCTCTGCCCCAGGGGGCTGCC
CTCTGAGGAATTCTCTGCTGAGAACATAGATAATGCTCTGATATCAGACATATGTGGG
GCTGCTGCCAACAGGGGAGTAATCAGCAACTCAGGGGACCTGTACGAGCTATAGCTTAC
TGGCTGAGAAAACATTCTCTGCTAGATGGCAATGGCATCCAGTCTCAATGCTTCTAGAT
GGTCGCTCTTTCACAGTAACAAAGGCAAAGTAGTACACAGGAGGCCACAGGACAAGCA
GTGTCACAGCACATCCACCAACAGGTAACAGCTAACAGAAAACACCCGAGAAGAAAATGG
CAATAAAGATTGTAAGCAGACATTGCAATTCTGATTGATGGAAGCTTAATATTGGCAGC
GGCGATTAAATTACAGAAGAAATTGTTGGAAAGTGGCTTAATGTTGGGAATTGGAAACA
GAAGGACCAACATGTGGGCTGTTAACGCAGTGAAACATCCAAAATAGAATTAACTGTAA
AAACTTTACATCAGCCAAAGATGTTTGTGCCCCATAAAGGAAGTAGGTTCAAGGGGTTA
ATTCCAATACAGGAAAGCCCTGAGCAACTCTGCTCAGAACATTCTCACGGTAGATGCTGG
GTAAGAAAAGGGATCCCCAACATGGTGGGGTTATTATGATGGTTGGCCTTGTGACAT
CGAGGAAGCAGGCATTGTGGCAGAGAGTTGGTGTCAATGATTATAGTTCTGTGCCCC
AGCCTATCCCTGAAGAACATGGGGATGGTCAGGATGTACACATTGTTGACAAGGCTGCTGT
CGGAATATGGCTCTTCTTACACATGCCAACACTGGTTGGCACCACAAAATACGTTAA
GCCCTGTTGACAGAACGCTGCACTGTACGAAACATGATGTGCAAGAACCTGTTAACT
CACTGAACATTGCCCTTCTAATTGATGGCTCCAGCAGTGGGAGATGCAATTCCGCCCTC
ATGCTGTAATTGTTCCAACATGCCAACACTTTGGAAATCTGGACATTGGTGCCAGAT
ACCTGCTGTAACGTTTACTTATGATCAGCGCAGGGAGTCTAGTTCACTGACTATAGCACCA
AAAGAGAATGTCTCATGCTGACGAAACATCGGCTATATGAGTGGTGGAACAGCTACTGGT
GATGCCATTCTCTTCACTGTTAGAAATGTTGGCCCTATAAGGGAGAGCCCCAACAGAA
CTTCCCTAGTAATTGTCACAGATGGGAGTGGCAGTCTTATGATGATGTCCAGGGCTCTGAGCTGCTG
CACATGATGCCAGGAATCACTATCTTCTGTTGGTGTGGCTGGCACCTCTGGATGACCTG
AAAGATGCTCTTAAACCGAAGGAGTCTCACGCTTCTTCAAGAGAGTTCAAGGATT
AGAACCAATTGTTCTGATGTCATCAGAGGATTGTAAGAGATTCTTAGAATCCAGCAAT
ATGGTAACATTGACAACTTGAAAGAAAAGTACAAGGGGATCCAGTGTGAAATTGTATT
CTCATAAATCTGAAATGCTTACATGACTAGAATCAGATACAAACTATTAGTATGTCAC
AGCCATTAGGCAAAACTGCTGAGGCTTCAATCATGGCTTCTGAGAACACTGAGAA
ACTTTGGTAAAAAAACACTGCTGAGGCTTCAAGGTTCAACCTGCTACTAAATGTA
GATAATGTGATTAAAAACCTTAAGGTTCAACCTGCTACTAAATGTA
TTCCATAGCTCAATAAAAGAATCTGATACTTAGACCAAAAAAAA

FIGURE 82

MSAAWI PALGLGVCLLLLPGPAGSEGAAPIAITCFTRGLDIRKEKADVLCPGGCPLEEFSVY
GNIVYASVSSICGAAVHRGVISNSGGPVRVYSLPGRENYSSVDANGIQSQMLRSASFTVT
KGKSSTQEATGQAVSTAHPPTGKRLKKTPPEKKTGNKDCDIAFLIDGSFNIGQRRFLNLQKN
FVGKVALMLGIGTEGPHVGLVQASEHPKIEFYLKNFTSAKDVLFAIKEVGFRGGNSNTGKAL
KHTAQKFFTVDAGVRKGIPKVVVVFIDGWPSSDIEEAGIVAREFGVNVFIVSVAKPIPEELG
MVQDVTFVDKAVCRNNGFFSYHMPNWFGETTYVKPLVQKLCTHEQMMCSKTCYNSVNIAFLI
DGSSSVGDSNFRLMLEFVSNIAKTFEISDIGAKIAAVQFTYDQRTEFSFTDYSTKENVLA
RNIRYMSGGTATGDAISFTVRNVFGPIRESPNKNFLVITDQSYDDVQGPAAAHDAGITI
FSVGVAWAPLDDLKDMASKPKESHAFFTREFTGLEPIVSVDVIRGICRDFLESQQ

09902615-071000

Signal sequence:

amino acids 1-24

N-glycosylation site.

amino acids 100-104, 221-225

Casein kinase II phosphorylation site.

amino acids 102-106, 129-133, 224-228, 316-320, 377-381, 420-424,
425-429, 478-482, 528-532

N-myristoylation site.

amino acids 10-16, 23-29, 81-87, 135-141, 158-164, 205-211,
239-245, 240-246, 261-267, 403-409, 442-448, 443-449

Amidation site.

amino acids 145-149

FIGURE 83

CCGGCGCCTCCCGCACCGCGGGCCACCGCGCCGCTCCCGCATCTGCACCCGAGCCC
GGCGGCCCTCCGGCGGGAGCGAGCAGATCAGTCAGCTGGCCCGCAGCGCAACTCGGTCCAGTC
GGGCGGGCGCTGCGGGCGCAGAGCGGAAGATGCAAGCGCTTGGGCCACCTGCTGCTGCTGC
TGCCTGGCGCGGGTCCCCACGGCCCCCGGCCGCTCGACGGCAGCTCGGCTCAGTC
AAGGCCGGCCGGCTCAGCTGGCAGAGGAGGGCACCCCTAATGAGATGTTCCGGCGA
GTTGAGGAACGTGATGGAGGACACGCAGCACAAATTGCGCAGCGCGTGGGAAGAGATGGAGG
CAGAAGAAGCTGCTGCTAAAGCATCTAGAAGTGAACCTGGCAAACATTACCTCCAGCTAT
CACAAATGAGAACCAACACAGAACAGAAGGTTGAAATAATACCATCCATGTGCACCGAGAAAT
TCACAAGATAACCAACAAACAGACTGGACAGGTTCTTCAGAGACAGTTACATCATCTG
TGGGAGACGAAGAAGGGCAGAAGGGCACAGACTGGCATCATGCAGCAGGACTGTGGCCCGAGC
ATGTAAGTGCAGTTGCCAGCTTCAGTACACCTGCCAGGCATGCCGGGCCAGGGATGCT
CTGCAACCGGGAGACAGTGAAGTGTGGAGACCCAGCTGTGTCTGGGTCACTGCACAAAA
TGGCCACCAAGGGAGCAGAATGGGACCATCTGACAAACAGAGGGACTGCCAGCGGGCTG
TGCTGTGCCCTTCAGAGAGGCTGCTGTTCTGTGTCACACCCCTGCCGTGGAGGGCGA
GCTTGTGCCATGACCCCCAGGCCGCTCTGGACCTCATCACCTGGAGCTAGAGCTGATG
GAGCCCTTGGACGATGCCCTTGTGCCAGTGGCCCTCTGCCAGCAGGCCACAGGCCACAGCTG
GTGTTATGTGCAAGCCGACCTCTGTGGGAGCGCTGACCAAGAGTGGGAGATCTGTGCC
CAGAGAGGCTCCCGATGAGTATGAAGTGTGGCAGCTTCATGGAGGAGGTGCGCAGGAGCTGG
AGGACCTGGAGAGGAGGCTGACTGAAGAGATGGCAGCTGGGGAGCCTGCCGTGCCGCT
GCACACTGCTGGGGAGGGAGAGATAATTTAGATCTGGACAGGCTGTGGTAGATGTGCAATAGAA
ATAGCTAATTATTCAGGTGTTGCTTGTGGCTTGTGACAGGCTTCTCACA
TCTCTTCCCAGTAAGTTCCCTCTGGCTTGACAGCATGGGTGTTGCAATTGTTCTCAGC
TCCCGGAGCTGTTCTCCAGGCTTCACAGTCTGCTGGAGAGTCAGGCGAGGGTTAAAC
TGCAGGAGCAGTTGCTCCACCCCTGTCAGATTATTGCTGCTTGTGCTCTACAGTTGGCAG
ACAGCGGTTGTTCTACATGGCTTGTATAATTGTTGAGGGAGGAGATGGAAACAATGTG
AGTCTCCTCTGATGGTTTGTGGGAAATGTGGAGAAGAGTGGCTGCTTGCACAAATCAA
CTGGCAAAATGCAACAAATGAATTTCACCCAGGCTTCTTCCATGGCATAGGTAAGCTG
TGCCTTCAGCTGTTGCAAGATAATTGTTCTGTTACCCCTGCAATTACATGTGTTATTCTAC
AGCAGTGTGCTCAGCTCTACCTCTGTGCGAGGGCAGATTTCATATCCAAGATCAATT
CCTCTCAGCACAGCCTGGGGGGTCAATTGTTCTCTGCTCCATCAGGGATCTCAGAG
GCTCAGAGACTGCAAGCTGCTTGCACAGTCAACAGCTAGTGAAGACAGCAGCAGTTCT
CTGGTTGTGACTCTAAGCTCAGTGCCTCTCCACTACCCACACAGCTTGGTGCACCAA
AAGTGTCTCCAAAAGGAAGGAGAATGGGATTTTCTTGAGGCATGCACATCTGGAAATTAG
GTCAAAACTAATTCTCACACCTCTAAAGTAACACTACTGTTAGGAACAGCAGTGTCTC
AGTGTGGGGCAGCGTCTCTTAATGAAGACAATGATATTGACACTGTCCTCTTGGCAGT
TGCATTAGTAACCTTGAAAGGTATATGACTGAGCGTAGCATACAGGTTAACCTGCAGAAAC
GTACTTAGGTATTGTAGGGCAGGGATTAAATGAATTTGCAAACATCATTAGCAGCAAC
TGAAGACAATTATCACCAACAGGAGAAATCAACCCAGCAGCAGGGCTGTGAAACATGTT
GTAATATGCGACTGCGAACACTGAACTCTACCGCAGCTCCACAAATGATGTTTCAGGTGTCA
TGGACTGTTGCCACCATGTATTCTACAGAGTTCTTAAAGTTAAAGTTGACATGATGTTA
TAAGCATGCTTTCTTGAGTTAAATTATGATATAAACATAAGTGCATTAGGCAATTAGAA
ATAATCACTCAACTGCACAAAAAA

FIGURE 84

MQRLGATLLCLLLAAAVPTAPAPAPTATSAVVKPGPALSYPQEEATLNEMFREVEELMEDTQ
HKLRSAVEEMEAEEAAAKASSEVNLANLPPSYHNETNTDKVGNNTIHVREIHKITNNQTG
QMVFSETVITSVGDEEGRRSHECI IDEDCGPMYCFQASFQYTCQPCRGQRMLCTRSECCG
DQLCVWGHCTKMATRGSGNTICDNQRDCQPGLCQFQRGLFPVCTPLPVEGELCHDPASRL
LDLITWELEPDGALDRPCASGLLCQPHSHSLVYVCKPTFVGSRDQDGIEILLPREVPDEYEV
GSFMEEVRQELEDLERSLTEEMALGEPAAAAALLGGEI

Signal sequence:

amino acids 1-19

N-glycosylation site.

amino acids 96-100, 106-110, 121-125, 204-208

Casein kinase II phosphorylation site.

amino acids 46-50, 67-71, 98-102, 135-139, 206-210, 312-316,
327-331

N-myristoylation site.

amino acids 202-208, 217-223

Amidation site.

amino acids 140-144

00902615-071001

FIGURE 85

FIGURE 86

MRLLVAPLLAWVAGATATVPVVPWHVCPQQCACQIRPWTPRSSYREATTVDCLDLFLTA
VPPALPAGTQTLQQNSNSIVRDQSESLGYNLNLTELDLSQNSFSARDCDCDFHALPQLLSSLHL
EENQLTRLEDHSFAGLSQLYELVNHQLYRIAPRAFSGLSNLLRHLNSNLLRAIDSRWFE
MLPNLIELMIGGNKVDAILDMNFRPLANRLSVLVAGMNLRETSDYALEGLQSLESLSYFDNQ
LARVPRRALEQVPGLKFLDLNKNPLQRVPGDFANMLHLKELGLNNMELVSLDKFALVNL
ELTKLDTINNPRLSFIHPRAFHHLQPMETLMLNNNNNALSALHQQTVESLPNLQEVGLHGNPIR
CDCVIRWANATGTRVRFIEPQSTLCAPPDLQRQLPVREVFPFREMTDHCLPLISPRSFPPPSLQ
VASGESMVLHCRALAEPEPEIYVWTPAQLRPTAHPAGRRYRVPEGTLERLRTVAEEAGLYT
CVAQNLVGADTKTUVVVGRALLQPGRDEGOGLELRVQETHPYHILSLWVTPPNTSTNLTW
SSASSLRQGATALARLPRGTHSYNITRLLCQATEWACLQVAFADAHTQALACVWARTKEATS
CHRALGDRPGLIAILALAVVLLAAGLAHLGTCQPKRGVGGRRPLPPAWAFWGWGSAFSPVRRV
SAPLVLWPWNPGRKLPRSSGETLPLPSONS

Signal sequence:

amino acids 1-18

Transmembrane domain:

amino acids 629-648

N-glycosylation site.

amino acids 94-98, 381-385, 555-559, 583-587

cAMP- and cGMP-dependent protein kinase phosphorylation site

amino acids 485-489

Casein kinase II phosphorylation site.

amino acids 46-50, 51-55, 96-100, 104-108, 130-134, 142-146, 243-247, 313-317, 488-492, 700-704

Tyrosine kinase phosphorylation site.

amino acids 532-540

N-myristoylation site

amino acids 15-21: 493-499 566-573

Amidation site

amino acids 470-474, 660-664, 692-696

FIGURE 87

GCAGGCCAAGGCGCTGTTGAGAAGGTGAGAAGAAGTCGGGACCCATGGAGGGGAGACATTGTGACCGCT
CTACATCGGCAGACCATCATCAAGGTGATCAAGTTCATCCCTCATCATCTGCTACACGGCTACTACGTGACAA
CATCAAGTTCGAGCTGGACTGCACCGTGGACATTGAGAGGCTGACGGCTACCGCACCCTACCGCTGTGCCACCC
CTGGCCACACTCTCAAGATCCTGGCTCTTCAAGAAGTACTGTTGAGTCATCGTGTGAGGAGAGCAGCTACAG
CACACTGGTGGGATGCTACGGCCTCCTCAAGAAGTACTGTTGAGTCATCGTGTGAGGAGAGCAGCTACAG
CGACATCCCGAGCTCAAGAACGACTTGGCTTCACTGGTGGACCTCAAGCTGACGGCTGACCCCTCATCTCCAA
GCCCTTCTGGCGTCTTCTGGAGGTGAGTGAAGAACAGCTGCGCAGCTGACCTGTCAGTCTAGTGGCAT
GGACAAGCTCCGGAGCGGCTCACAAAGAACCGCAGGAGCTGGAGCTGACCCCTCATCTCCAGTGGCAT
CCCTGACACTGTGTTGACCTGGTGGAGCTGGAGCTGAGCTGGCTTACACACAGCGCCAAAGATGAAGCGCTCGCGT
CAGCATTGCCCCAGTCAAGGGCCCTCAAGAGACTGGCTTACACACAGCGCCAAAGATGAAGCGCTCGCGT
GGCCCTCTCGGGAGAAGCTTCGGGGCGCTCACATCAAGTCAAGGACATCAAGGGAGATCAGGAGATCTGAGATCTA
TAGCCAGAACAGACTGGAGGAGCTGCACCTGGCGCAACCTTGAGGGAGAACACCGCTACATGTCATCGA
CGGGCTGGGAGACTAAACGCCCTCAAGGTGCTGGGCTCAAGAGCAACTAACGAGCTGGCCACAGGGTGTAC
AGATGTGGCGTGCACCTGCAAGACTGTCATGGCTGAGCTGGCCACCTGAGCTCATCTGGCTTCAACAGCCTAA
GAAGATGGCGAACCTGACTGAGCTGGAGCTGAGCTGGCCACCTGGAGCTGGCCACCTCCATCTGGAGCT
CCACACCTGAGGAGATTCAAGGACAAACCTCAAGGACATCAAGGAGATCATGAGCTTCCAGGACACCT
GCACCGCTCACCTGGCTTACGGTGTGATCACACCATGCGCTACATCCCATGAGATCGGCAACCTCAAA
CTGGAGGCGCTTACCTGGACCCAAAGATGAGAAGATCTCCACCCAGCTCTCTACTGCGGCAAGCTGG
CTACACTGGACCTCAGGCCAACAAACACTGACCTTCTCTGGCGACATGGCTCTGGAGAACCTCCAGAACCT
AGCCATCACGGCAACCGGATGAGAGGCTCCCTCCGGAGGCTTCCAGGATGGCGAACCTGGCCCTCGACCT
GGGCAACAGTCAGTCACTGGCTTCCAGGGTGGGAGCTGAGGACCAACTGAGCAGATCGAGCTGGGG
CAACCGCTGAGTGGCTTGCCCTGGAGCTGGCCACCTGCTCAAGCGCAGCGCTTGGTGGTGGAGGA
GGACCTGTTCAACACTGGGACCCAGGAGTGAAGGAGGGCTGTGGAGGGCTGACAAGGAGCAGGCTGGAG
GGCCGGGAGCAGCACAGCAGGGAGCCCTGGCAGCTGGGAGGGAGGGAGCTGGAGCTTCTCCAG
AACTCCGGAGCAGCAGGAGACAGCTCCGGCTGGGAGGGAGCTGGGAGGGAGGGAGCTGGAGCTTCTCCAG
GGAGCTGATCTGTGGGGCTTCTCCCTGGGAGGGAGCTGGGAGGGAGGGAGCTGGAGCTTCTCCAG
AGCAACTCTCAAGGGCAGTATTGGGATAATCAGGGTCTCTGGGAGGGAGCTGGGAGGGAGCTGGAGCT
CTGGGAGGGAGGGAGGGAGGGAGGGAGGGAGGGAGGGAGGGAGGGAGGGAGGGAGGGAGGGAGGGAG
AGATAACTTATCACTTCAAGAAGTTCAGGGAGGGAGGGAGGGAGGGAGGGAGGGAGGGAGGGAGGGAG
TTGTCCTTATTTAGCGATGCGCGGGCATTAAACACCCACTGGACTTCAGCAGAGTGGCTGGGGGGAG
CCATGGGAGGGTCCAGCCAGTGGGGGGGGCTGGGCTGGGAGGGAGGGAGGGAGGGAGGGAGGGAG
AAGGGCAGGGCTGGAGCTTCTCTGGTGGGAGGGAGGGAGGGAGGGAGGGAGGGAGGGAGGGAGGGAG
AAACAACTTTTTTTAAAAAAAGCTTTGAAAATGGATGGTTGGGTTATTTAAAGAAAAAAACTTAAAAAA
AAAAGACACTAACGGCAGTGGAGTGGGAGGGTCTGGGAGGGAGGGAGGGAGGGAGGGAGGGAGGGAG
TGAACTGTGTTCTTCTTCTCCCTGGGGCAGGGTGAGGGTGTCTGGGAGGGAGGGAGGGAGGGAGGGAG
CTATTGGTCTCTGGGGAGGGAGGGAGGGAGGGAGGGAGGGAGGGAGGGAGGGAGGGAGGGAGGGAG
ATGTGCTTGGCAGGACTCATTTCTGTTGGCTGTCGGCCAGAGGGAAATGGTCTGGAGCTGCCAAGGGAGGGAG
ACTGGGGTGGCTAATCCCGGGATGACCGGGTGTCTGGGCTCACTTCCACCTCCCTCTGGCTGCCCTGGCT
CGCACAGTGTAAAGGAGGACCAAGGAGGACCTGGCCAGACTTGTGTTCTCCCTCTGGGAGGGAGGGAG
CCAGTGGCACCAGCTGGGCTCGCTTCCATCAGGCCCTGGCTGCCACCTGGCTCTCATGAAGAGCAGACACT
GAGGGCTGGTGGGAGGGAGGGAGGGAGGGAGGGAGGGAGGGAGGGAGGGAGGGAGGGAGGGAGGGAG
CTGGAGTGACACAGGCCAGTGGCAGGACTGGTGGGAGGGAGGGAGGGAGGGAGGGAGGGAGGGAGGGAG
AGAAGGGTCCCGGCTTGGAGTCAATCACGTTGGAGACTAAGGGAGGGAGGGAGGGAGGGAGGGAGGGAG
CCATGGCTGTGGCTCATTTGTGTTCTGGCTGTGTCATGGATATAATCTCAAGAAATAATGACACTAG
CCTCTGACAACCATGAGAAGAAAAATCGGTACATGTGGGCTGTAAGTGGAGCTGGTACAGTCAAGTCAAA
ATCTATAACAGAAAAAA

FIGURE 88

MRQTIIKVIKFILIICTVYVHNIFKFDVDCTVLDIESLTYRCAHPLATLFKILASFYI
SLVIFYGLICMYTLWWMLRSLKKYSFESIREESSYSDIPDVKNDFAFMLHLIDQYDPLYSK
RFAVFLSEVSENLRLRQLNLNEWTLDKLRQRLTKNAQDKLELHLFMLSGIPDTVFDLVELEV
LKLELIPDVТИPPSIAQLTGLKELWLYHTAAKIEAPALAFRLRENLRALHIKFTDIKEIPLWI
YSLKTLLEELHLTGNLSAENNRYIVIDGLRELKRLKVLRLKSNLSKLPQVVTDVGVHLQKLSI
NNEGTLKLIVLNSLKKMANLTELLELIRCDLERIPHISIFSLHNLQEIDLKDNNLKTIEEIISFQ
HLHLRLTCLKLWYNHIAYIPIQIGNLTNLERLYLNRNKEIEKIPTQLFYCRKRLRYLDLSSHNNLT
FLPADIGLLQNLQNLAITANRIETLPPPELFQCRKRLRALHLGNNVLQSLPSRVGELETNLTQIE
LRGNRLECLPVELGECPLLKRSGLVLVEEDLFNTPPEVKERLWRADKEQA

099026133-071001

Transmembrane domain:

amino acids 51-75 (type II)

N-glycosylation site.

amino acids 262-266, 290-294, 328-332, 396-400, 432-436, 491-495

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 85-89

Casein kinase II phosphorylation site.

amino acids 91-95, 97-101, 177-181, 253-257, 330-334, 364-368,
398-402, 493-497

N-myristoylation site.

amino acids 173-179, 261-267, 395-401, 441-447

FIGURE 89

GCCTGTTGCTGATGCTGCCGTGCGGTACTTGTCATGGAGCTGGCACTGCGCGCTCTCCGT
CCCGCGGTGGTTGCTGCTGCCGTGCTGGCTGAACGCAAGGAGCTGTATTGACT
GGCCCACAGAGGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCCTACATG
TTCTGGTGGCTTATTATGCCACCAACTCTGCAAGAACTTCAGAACTGCCCCGTGGTCAT
GTGGCTTCAGGGCGGTCCAGGGCGTTCTAGCACTGGATTGGAAACTTGAGGAATTGGC
CCCTTGACAGTGATCTAAACACAGGAAACCACCTGGCTCCAGGCTGCCAGTCTCCTATT
GTGGATAATCCGTGGGCACTGGGTTAGTTATGTGAATGGTAGTGGTGCCATGCAAGGA
CCTGGCTATGGTGGCTTCAGACATGATGGTCTCTGAAAGACCTTCTCAGTTGCCACAAAG
AATTCCAGACAGTCCATTCTACATTTCAGAGTCTATGGAGGAAATGGCAGCTGC
ATTGGTCTAGAGCTTATAAGGCATTAGCGAGGGACCATCAAGTCAACTTGGGGGT
TGCCCTGGGTGATTCTGGATCTCCCTGTTGATTGGTCTCCTGGGACCTTACCTGT
ACAGCATGTCCTCTCGAAGACAAAGGTCTGGCAGAGGTCTAAGGGTGCAGAGCAAGTA
CTGAATGCCGTAATAAGGGCTCTACAGAGAGGACAGAGCTGTGGGGAAAGCAGAAAT
GATCATTGAACAGAACACAGATGGGTGAACTTCTATAACATCTTAACTAAAGCACTCCCA
CGTCTACAATGGAGTCGAGTCAGAATTCAACAGAGCCACCTAGTTGCTTTGTCAAGCC
CACGTGAGACACCTACAACAGAGATGCCCTAAGGCCAGCTCATGAATGGCCCCATCAGAAAGAA
GCTCAAAATTATTCTGAGGATCAATCTGGGAGGCCAGGCTACCAACGTCTTGTAACA
TGGAGGAGGACTTCATGAAGCCAGTCATTAGCATTGTGGACGAGTTGCTGGAGGCAGGATC
AACGTGACGGTGTATAATGGACAGCTGGATCTCATCGTAGATACCATGGTCAGGAGCCCTG
GGTGGGAAACTGAAGTGGCCAGAACTGCCTAAATTCACTGCTTGTCAAGTCTACAGA
ACACTGACCCCTAAATCTTGGAAACATCTGCTTGTCAAGTCTACAGA
TACTGGATTCTGAAAGCTGGTCAATGGTCTCTGACCAAGGGACATGGCTCTGAAGAT
GATGAGACTGGTGACTIONAGAATAGGATGGATGGGCTGGAGATGAGCTGGTTGGCCT
TGGGGCACAGAGCTGAGCTGAGGCCGCTGAAGCTGTAGGAAGCGCCATTCTTCCCTGTATCT
AACTGGGCTGTGATCAAGAAGGTTCTGACCACTCTGACAGGATAAAATCATTGCTCT
GGAGGCAATTGGAAATTATTCTGCTTCTTAAACCTAAGATTAAATTGAT
TTGTTTTGATCAAAATAAGGATGATAATAGATATTAA

FIGURE 90

MELALRRSPVPRLLLLPPLLGLNAGAVIDWPTEEGKEVWDYVTVRKDAYMFWWLYYATNSC
KNFSELPLVMWLQGGPGGSSTGFGNFEIIGPLDSLKPRKTTWLQAASLLFVDNPVGTGFSY
VNGSGAYAKDLAMVASDMMVLLKTFFSCHKEFQTVPFYIFSESYGGKMAAGIGLELYKAIQR
GTIKCNFAGVALGDSWISPVDVLSWGPYLYSMSLLEDKGGLAEVSKVAEQVNAVNKGLYRE
ATELWGKAEMIIIEQNTDGVNFYNILTKSTPTSTMESSLEFTQSHLVCLCQRHVRHLQRDALS
QLMNGPIRKKLKIIPEDQSWGGQATNVFVNMEEDFMKPVISIVDELLEAGINVTVYNGQLDL
IVDTMGQEAWVRKLWPELPKFSQLKWKALYSDPKSLETSAFVKSYKNLAFYWILKAGHMVP
SDQGDMALKMMRLLVTQQE

TOP/OUT = SIDE/20060501

Signal sequence:

amino acids 1-25

N-glycosylation site.

amino acids 64-68, 126-130, 362-366

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 101-105

Casein kinase II phosphorylation site.

amino acids 204-208, 220-224, 280-284, 284-288, 351-355, 449-453

N-myristoylation site.

amino acids 22-28, 76-82, 79-85, 80-86, 119-125, 169-175,
187-193, 195-201, 331-337, 332-338, 360-366

FIGURE 91

GGCGCGGGAGAGGAGGCCATGGCGCGCGCGGGCGCTGCTGCTGGCGCTGCTGGCT
GGCTGGACTCAGGAAGCCGGAGTCGCAGGAGGCGGCCGCTTATCAGGACCATGCGGCCA
CGGGTCATCACGTCGCGCATCGTGGTGGAGAGGACGCCAACCTGGCGTTGGCGTGG
GGGAGGCCCTGCGCCTGTGGGATTCCCACGTATGCGGAGTGAGCCTGCTCAGCCACCGCTGG
CACTCACGGCGCGCACTGCTTGAACCTATAGTGACCTTAGTGATCCCTGGGTGGATG
GTCCAGTTGGCAGCTGACTTCCATGCCATCCTCTGGAGCCTGCAGGCCTACTACACCCG
TTACTCGTATCGAATATCTATCTGACGCCCTCGTACCTGGGAATTCACCTATGACATTG
CCTTGGTGAAGCTGTCTGCACCTGTACACTAAACACATCCAGCCCATCTGTCTCCAG
GCCCTCACATTGAGTTGAGAACCGGACAGACTGCTGGGTGACTGGCTGGGGTACATCAA
AGAGGATGAGGCAGTGCATCTCCCCACACCCCTCCAGGAAGTTCAGGTGCCATCATAAAC
ACTCTATGTGCAACCACCTCTCTCAAGTACAGTTCCGAAGGACATTTGGAGACATG
GTTTGTGCTGGCAACGCCAACGGCGGAAGGAGTCCTGCTCGGTGACTCAGGTGGACCCCTT
GCCCTGTAACAAGAATGGACTGTGGTATCAGATTGGAGTCGTGAGCTGGGAGTGGCTGTG
GTCGGCCCAATCGGCCCGGTGTCTACACCAATACAGCCACACTTGTGGATCCAGAAG
CTGATGGCCCAGAGTGGCATGTCAGGCCAGACCCCTCTGGCCACTACTCTTTCCCTCT
TCTCTGGGCTCTCCACTCTGGGCCGGTCTGAGCCTACCTGAGGCCATGCAGCCTGGGC
CACTGCCAAGTCAGGCCCTGGTCTCTCTGTCTTGGATAAAACACATTCCAGTTGA
TGCCCTTGCAGGGCATTCTTCAAAAAAAAAAAAAAAAAAAAAAA

09902515-071001

FIGURE 92

MGARGALLLALLLARAGLRKPESQEAAPLSGPCGRRVITSRIVGGEDAEELGRWPWQGSLRLW
DSHVCGVSLLSHRWALAAHCFETYSSDLSDPSGWMVQFGQLTSMPSFWSLQAYYTRYFVSN
YLSPRYLGNSPYDIALVKLsapVTYTKHIQPICLQASTFEFENRTDCWVTGWGYIKEDEALP
SPHTLQEVLQVAAIINNSMCNHLFLKYSFRKDIFGDMVCAGNAQGGKDACFGDSGGPLACNKNG
LWYQIGVVSVVGCGCRPNRPGVYTNISHHFEWIQKLMAQSGMSQPDPSWPLLFFPLLWALPL
LGPV

Signal sequence:

amino acids 1-18

N-glycosylation site.

amino acids 167-171, 200-204, 273-277

Casein kinase II phosphorylation site.

amino acids 86-90, 134-138, 161-165, 190-194, 291-295

N-myristoylation site.

amino acids 2-8, 44-50, 101-107, 225-231, 229-235, 239-245,
259-265, 269-275

Amidation site.

amino acids 33-37

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 252-263,

Serine proteases, trypsin family, histidine active site.

amino acids 78-84

FIGURE 93

CCCCACCGTCCCGGGACCGTGAAAAGGGCAGA**ATGGGACTCCAAGCCTGCCTCTAGGGCT**
CTTTGCCCTCATCCTCTCTGGCAAATGCAATTACGCCGGAGCCCGAACAGCGGGAGACGC
TGCCCCCAGGCTGGGTCTCTGGCCCTGGGGCGACCTGAGGAAGAGCTGAGTCTCACCTT
GCCCTGAGACAGCAGAAATGGGAAAAGACTCTCGGAGCTGGGTGAGGCTGTGCGATCCCCAG
CTCTCCTCAATACGGAAAATACCTGACCCCTAGAGAATGGGTGATCTGGTGGAGGCAATCCC
CACTGACCCCTCCACACGGTGCAAAATGGCTCTGGCAGGCCGGAGCCAGAACAGTGCCT
GTGATCACACAGGACTTCTGACTTCTGCTGAGCATCGAACAGCAGCTGCTGCT
GGGGCTGAGTTCATCACTATGGGAGGACCTACGAAACCCATGGTAAAGGTCCCCAC
ATCCCTACCCAGCTTCCACAGGCCCTGGGGCCCATGGGACTCTGGGACTGCACCGT
TTTCCCCAACATCATCCTCTGGCAAGCTCTGAGGCCAGGTGACACGGGACTGTAGGGCT
GCATCTGGGGTAACCCCTCTGTGATCGGAAAGCATAACACTGACCTCACAAAGCTGG
GCTCTGGCACCAGCAATAACAGCCAAGGCTGTGCCAGTCTCTGGAGCAGTATTTCCATGAC
TCAGAGCTGGCTCAGTCTAGCCTCTGGGGCAACATTTGCACATCGGGCATCAGTAC
CCGGTGTGGTTGACAAACAGGGCGGGGGCGGGGGGGATTGGAGGCAAGCTAGATGTGCACT
ACCTGATGAGTGTGGTGCACATCTCACCTGGGTCTACAGTAGCCCTGGCCGGCATGAG
GGAGCAGGAGCCCTCTGCACTGCTCAGTGTGAGTCAAGCCTGCCCCATGT
GCATACTGTGAGCTATGGAGATGAGGACTCCCTCAGCAGGCCCTACATCCAGGGCTCA
ACACTGAGCTCATGAAGGCTGCCGCTCGGGCTCACCTGCTCTGCCCTCAGGTGACAGT
GGGGCCGGGTGTGGTCTCTGGAGAACACCCAGTCTCCGGCTTACCTTCCCTGCCCTCAG
CCCTATGTACACAGTGGAGGACATCTCCAGGAACCTTCCATCACAAATGAAA
TTGTTGACTATATCAGTGTGGTGCCTCAGCAATGTTCTCCAGGCCCTCATACAGGAG
GAAGCTGTAACGAAGTCTCTGAGCTCTAGCCCCCACCTGCCACCATCAGTTACTCTCAATGC
CAGTGGCCGCTGCCACCCAGATGTTGCTGCACTTCTGATGGCTACTGGGTGAGCAACA
GAGTGGCCCATTCATGGGTGCTCGGAGACCTGGCCCTACTCCAGTGTGGGGGATCTA
TCCCTGATCAATGAGCACAGGATCCTTAGTGGCCGCCCCCTCTGGCTTCTCACCCAAG
GCTCTACCGAGCACAGGCTCTGGATGTAACCCGTCAGGCTGCCATGAGTCTGTC
TGGATGAAAGAGCTAGAGGGCAGGGTTCTGCTCTGGCTGGGATCTGTAAACGGC
TGGGGAAACACCAACTCTCCAGCTTGCT**TGAAGACTCTACTCAACCCCTGACCCCTTCTATC**
AGGAGAGATGGCTTGTCCCCCTGCCCCCTGAAGCTGGCAGTTAGTCCCTTATCTGCCCTGTTG
GAAGCCCTGCTGAACCCCTCAACTATTGACTGCTGCAGACAGCTTATCTCCAAACCCCTGAAA
TGCTGTGAGCTTGACTIONACTCCAACTTCCATGCTCATCATACTCAGGTCTCTTACT
CCTGCCCTAGATCCCTCAATAAGATGCTGTAACTAGCATTTTGATGCTCTCCCTCGC
ATCTCATCTTCTCTTCAATCAGGCTTCTCAAAGGGTTGATACAGACTCTGTGACTA
TTCACTCTGTATTCATTCCTCAACTTCACTGCAAGGAGACCTCTACTGTACCGTTTACTCT
TTCCTACCCCTGACATCCAGAAACATGGCTCCAGTGCTACTTCTCAATCTTGCTTATG
GCCCTTCCATCATAGTGTCCCCACTCCCTCTCTTACTTGACTIONCTCCAGGTCTTAACCTCTG
ACTACTTGTCTCTCCCTCTCATCAATTCTGCTCTCATGGAAATGCTGACCTCTCATG
TCCATTGTAGATTTGCTCTCTCAGTTACTCATTGTCCTGGACAAATCACTGACA
TCTACAACCACTTACCATCTCACTAAATAAGACTTCTATCCAATAATGATTGATACCTCAA
TGAAAAAA

FIGURE 94

MGLQACALLGLFALILSGKCSYSPEDQRRTLPGWVSLGRADPEEELSLTFALRQNVERLS
ELVQAVSDPSSPQYGKYLTLLENVALVRSPSLTLHTVQKWLAAAGAQKCHSVITQDFLTCWL
SIRQAELLPGAEFHHYVGPPTEHVVRSRPHYQLPQALAPHVDFVGGHLRFPPPTSSLRQRP
EPQVTGTVGLHLGVTPSVIRKRYNLTSDVGSGTSNNSQACAFQLEQYFHDSDLAQFMRLLFG
GNFAHQASVARVVGQQGRGRAGIEASLDVQYLMISAGANISTWVYSSPGRHEQCEPFLQWLML
LSNESALPHVHTVSYGDDEDSLSSAYIQRVNTELMAAARGLTLFASGDSGAGCWSVGRH
QFRPTFPASSPYTTVGGTSFQEPLITNEIVDYIISGGGFSNVFPRTSYQEEAVTKFLSSSP
HLPPSSYFNASGRAYPDVAALSDGYWVVSNRVPIPWVSGTSASTPVFGGILSLINEHRLSG
RPPPLGFLNPNRPLYQOHGAGLFDVTRGCHECLDDEVEGQGFCGSPGWDPVTGWTPTSQLC

Signal sequence:

amino acids 1-16

N-glycosylation site.

amino acids 210-214, 222-226, 286-290, 313-317, 443-447

Glycosaminoglycan attachment site.

amino acids 361-365 408-412 538-542

Casein kinase II phosphorylation site

amino acids 313-316 334-338 382-386 429-434 525-529

N-myristoylation site

amino acids 2-8, 107-113, 195-201, 199-205, 217-223, 219-225, 248-254, 270-276, 284-290, 409-415, 410-416, 473-479, 482-488, 521-527, 533-539, 549-555

FIGURE 95

TOP 10 STRAINS

GGCGCGCGCTCTCTCCGGGCCACACCTGTCTGAGCGCGCAGCGAGCGCGGCCGGC
GGCTGCTCGCGCGGAACAGTGTGCTCGCATGGCAGGGATTCCAGGGCTCCTCTTCTC
TTCTTCTGCTCTGTGCTGTGGCAAGTGTAGCCCCACTACAGTGCCCCCTGGAAACCCACTTG
GCCTGCATACCGCCTCCGTGCTTGCAGCTACCCCTCAATTAGCCAAGCCAGACT
TTGGAGCGAAGCCAAATTAGAAGTATCTCTCATGTGGACCCAGTGTCTATAAGGAACT
CCACTGCCACTTACGAAGAGGCCAAGCAATATCTGTCTATGAAACGCTATGCCAATGG
CAGCGCACAGAGACGCAGGTGGGATCTACATCCTCAGCAGTAGTGGAGATGGGCCAAC
ACCGAGACTCAGGGCTTCAGGAAAGTCTGAAGGAAGCGCAGATTATGGCTATGACGC
AGGTTCACTTTGGGAGGACTCTCTGCTCAACTACCCCTTCACATCAGTGAAGTT
ATCCACGGGCTGCACCGCACCCCTGGTGGCAGAGAACGATGCTCCTCACAGCTGCCACTGCA
TACACGATGGAAAAACCTATGTGAAAGAACCCAGAACGCTTCAGTGGCTTCTAAAGCC
AAAGTTAAAGATGGTGGTCAGGGGCCAACGACTCCACTCAGCCATGCCAGCAGATGAA
ATTTCACTGGATCCGGGTGAAACGCACCCATGTGCCAAGGGTTGGATCAAGGCAATGCCA
ATGACATCGGATGGATTATGATTATGCCCTCTGGAACTCAAAAGCCCCACAAGAGAAAA
TTTATGAAGATTGGGTGAGCCCTCTGCTAAGCAGCTGCCAGGGGCCAGAATTCACTTCTC
TGGTTATGACAATGACCGACAGGAATTGGTGTATCGCTTCTGTGACGTCAAAGACGAGA
CCTATGACTTGTCTACCAGCAATGCGATGCCAGCCAGGGGCCAGGGCTCTGGGTCTAT
GTGAGGATGTGGAAGAGACAGCAGCAGAACGTTGGAGCGAAAAATTATGGCATTTCAGG
GCACCACTGGGTGACATGAATGGTCCCACAGGATTCAACGTGGCTGTCAAATCACTC
CTCTCAAATATGCCAGATTGCTATTGGATTAAGGAAACTACCTGGATTGTAGGGAGGG
TGAACACAGTGTCCCTCTGGCAGCAATTAAAGGTCTTCATGTTCTATTAGGAGAGGCC
AAATTGTTTTGTCAATTGGCGTGACACAGTGTGTGTGTGTGTGTGTAAAGGTGT
CTTATAATCTTACCTATTCTACAATTGCAAGATGACTGGCTTACTATTGAAAATCG
GTTTGTGTATCATATCATATCATTAAGCAGTTGAAGGCATACTTTGCATAGAAATAA
AAAAAAACTGATTGGGCAATGAGGAATTGACAATTAAAGTTAACTTCACGTTTTG
CAAACATTGATTTTATTTCATCTGAATTGTTCAAAGATTATAATTAAATTGGCATA
CAAGAGATATGAAAAA

FIGURE 96

MAGIPGLLFLLFFLLCAVGQVSPYSAPWKPTWPAYRLPVVLPQSTLNLA
KPDFGAEAKLEVS
SSCGPQCHKGTPLYEEAKQYLSYETLYANGSRTETQVGIYILSSSGDGAQHRDSSGKS
RRKRQIYGYDSRFSIFGKDFLLNYPFSTSVKLSTGCTGTLVAEKHVLTA
AHCIHDGKTYVK
TQKLRVGFLLKPKFKDGGRGANDSTSAMP
EQMKFQWIRVKRTHVPKGWIKGNANDIGMDYD
A
LLELKPKPHKRKFMKIGVSPPAKQLP
GGRIHFGSYDNDRPGNLVYR
FCDVKDETYD
LLYQQCD
AQPGASGSGVYVRM
WKRQQQKWERK
IIGIFSGHQV
WDMNGSPQDFN
VAVRITPL
KYAQI
CYW
IKGNYLDCREG

Signal sequence:

amino acids 1-19

N-glycosylation site.

amino acids 93-97, 207-211

Glycosaminoglycan attachment site.

amino acids 109-113, 316-320

Casein kinase II phosphorylation site.

amino acids 77-81, 95-99, 108-112, 280-284, 351-355

N-myristoylation site.

amino acids 159-165, 162-168, 202-208, 205-211, 314-320, 338-344

Serine proteases, trypsin family, histidine active site.

amino acids 171-177

1000-230650

FIGURE 97

1001 0720-51920690

GCATGCCCTGGGCTCTCGAGCCTGCTGCCCTGCTCCCCCCCCACCAGCCATGGTGGTTT
CTGGAGCGCCCCCAGCCCTGGGCTGGGGCTGCTCGGCACCTCACCTCCCTGCTGCTGCTG
GCGTCGACAGCCATCCTCAATCGGGCAGGATACTGTTCCCCAGCCTGTGGGAAGCCCCA
GCAGCTGAACCGGGTTGGGGCGAGGACAGCACTGACAGCGAGTGGCCCTGGATCGTGA
GCATCCAGAAGAATGGGACCCACCACTGCGCAGGTTCTCTGCTCACCAAGCCGCTGGGTGATC
ACTGCTGCCCACTGTTCAAGGACAACCTGAACAAACCATACCTGTTCTGTGCTGCTGGG
GCCCTGGCAGCTGGGGAACCCCTGGCTCTGGTCCCAGAAGGTGGGTGGCTGGGCTGGGAGC
CCCACCCCTGTGATTCCCTGGAAGGAAGGTGCCCTGTGCAGACATTGCCCTGGTGCGTCTCGAG
CGCTCCATACAGTTCTCAGAGCGGGCCTGCCCATCTGCCCTACCTGATGCCCTATCCACCT
CCCTCCAAACACCCACTGCTGGATCTCAGGCTGGGGAGCATCCAAGATGGAGTCCCTTG
CCCACCCCTCAGACCCCTGCGAGAACCTGAAGGTTCTATCATCGACTCGGAAGTCTGCAGCCAT
CTGTACTGGCGGGAGCAGGACAGGACAGGGACCCATCACTGAGGACATGCTGTGCCGCTACTT
GGAGGGGGAGCAGGGATGTTGCTGGCGACTCCGGGGGGCCCTCATGTGCCAGGTGGACG
GCCCTGGCTGCTGGCCGCATCATCAGCTGGGCGAGGGCTGTGCCAGCGAACAGGCC
GGGGTCTACATCAGCCTCTGCGCACCGCTCTGGGTGGAGAAGATCGCAAGGGTGCA
GCTCCGCGGGCGCGCTCAGGGGGTGGGGCCCTCAGGGCACCGAGCCAGGGCTCTGGGCCG
CCCGCGCTCCAGGGCGCAGCGGACGCGGGCTGGATCTGAAAGGCGGCCAGATCCACA
TCTGGATCTGGATCTGCGCGGCCCTCGGGCGTTCCCGCGTAAATAGGCTCATCTACC
TCTACCTCTGGGGCCGGACGGCTGCTGCCAAAGGAAACCCCTCCCGACCCGCCGAC
GCCCTCAGGCCCCCTCCAAGGCATCAGGCCGCCAACGGCCTCATGTCCCCGCCAC
GACTTCCGGCCCCGGCCCCGGGGCCCAGCGCTTTGTTGATATAATGTTAATGATTTTAT
AGGTATTTGTAACCCCTGCCACATATCTTATTATTCTCCAATTCAATAATTATTATT
CTCCAAAAAA

FIGURE 98

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA43318
><subunit 1 of 1, 317 aa, 1 stop
><MW: 33732, pI: 7.90, NX(S/T): 1
MVVSGAPPALGGGCLGTFTSLLLLASTAILNAAIRPVPPACGKPQQLNRRVVGGEDSTDSEWP
WIVSIQKNGTHHCAGSLLTSRWRVITAHHCFKDNLNKPYLFSVLLGAWQLGNPGSRSQKVGVVA
WVEPHPVYSWKEGACADIALVRLERSIQFSERVLPICLDPASIHLPNNTHCWISGWGSIQDG
VPLPHPQTLQKLKVPIIDSEVCSSHLYWRGAGQGPITEDMLCAGYLEGERDACLGDGGPLMC
QVDGAWLLAGIISWGEGCAERNRPGVYISLSAHRSWVEKIVQGVQLRGRAQGGGALRAPSQG
SGAAARS

Signal sequence:

amino acids 1-32

N-glycosylation site.

amino acids 62-66, 96-100, 214-218, 382-386, 409-413, 455-459,
628-632, 669-673, 845-849, 927-931, 939-943, 956-960

Glycosaminoglycan attachment site.

amino acids 826-830

Casein kinase II phosphorylation site.

amino acids 17-21, 39-43, 120-124, 203-207, 254-258, 264-268,
314-318, 323-327, 347-351, 464-468, 548-552, 632-636, 649-653,
671-675, 739-743, 783-787, 803-807, 847-851, 943-947, 958-962,
1013-1017, 1019-1023, 1021-1025

Tyrosine kinase phosphorylation site.

amino acids 607-615

N-myristoylation site.

amino acids 179-185, 197-203, 320-326, 367-373, 453-459, 528-534,
612-618, 623-629, 714-720, 873-879

09902615 - 07/10/04

FIGURE 99

GACGGCTGCCACCATGCACGGCTCCTGCAGTTCTGATGCTCTGCTGCCCTACTGCTA
CTGCTGGTGGCCACCACAGGGCCGGTTGGAGCCCTCACAGATGAGGAGAAAGCTTGATGGT
GGAGCTGCACAAACCTCTACCGGGCCAGGTATCCCGACGGCCTCAGACATGTCGACATGA
GATGGGACGAGGAGCTGGCCGCCCTCGCCAAGGCCTACGCACGGCAGTGGCTGTGGGCCAC
AACAGGAGCGGGCGCCGGCGAGAATCTGTTGCCATCACAGACGAGGGCATGGACGT
GCCGCTGGCCATGGAGGAGTGGCACACAGCGTGTGAGCACTAACCTCAGCGCCGCCACCT
GCAGCCCAGGCCAGATGTGGCCACTACACGCAGGTGGTATGGCCAAGACAGAGAGGATC
GGCTGTTCCACTCTGTGAGAAGCTCAGGGTGTGAGGAGACCAACATGAAATTACT
GGTGTGCAACTATGAGCCTCCGGGAAACGTGAAGGGAAACGGCCCTACCGAGGAGGGACTC
CGTGCTCCAATGTCCTCTGGTACCGTCAAGAACCTCCCTCTGTGAACCCATCGGAAGC
CCGGAAAGATGCTCAGGATTGCTTACCTGTACTGAGGCCCATCCTCCGGGCACTGA
AGCATCAGACTCTAGGAAAATGGGTACTCCTCTTCCTAGCACAGGGGATTCCGGCTTCT
TGTTAACAGAGGTCTCAGGCTCCCTGGCAACCAAGGCTCTGCTGTGAAACCCAGGCC
CCAACCTCCTTAGCAACGAAAGACCCGCCCTCCATGGCAACAGAGGCTCACCTTGCCTAAC
AACTGAGGTCCCTCCATTGGCAGCTCACAGCCTGCCCTGGATGAGGAGGCCATTA
CCTTCCCCAAATGACCCATGTTCTATCCAAAATCAGCAGACAAAGTGCAGACAAAACA
AAAGTGCCCTCTAGGAGGCCAGAGAACTCTGACCCCAAGATGTCCTGACAGGGCAAG
GGAACCTCCTACCCATGCCAGGAGGAGGCTGAGGCTGAGGCTGAGTTGCCCTTCCAGTG
AGGCTTGGCTCAGTTTCCAGGCCAGGACAAGGCCAGGTGAGCTGCAGGCCACACTGGAC
CACACGGGGCACACCTCCTCCAAGTCCCTGCCCAATTCCCCAACACCTCTGCCACGCCAA
TGCCACGGGTGGCGTGCCTGGCTCTGCAGTCGCTCTGCCAGGTGAGGCCCTGACA
ACCTCTAGCGTTGTGTCAGGCTGAACCTGGCCCTGGCATGTTGGGCCCTCTGGGA
CTACTGCTCCTGCCCTCTGGTGTGGCTGAATCTCTGAATGGGATACCAACTCAAAGGG
TGAAGAGGTCACTGCTCTCTGTGATCTTCCCCACCCCTGCCCCAGCCCTAAACAAGATA
CTTCTGGTTAAGGCCCTCGGAAGGGAAAGGCTACGGGCATGTCCTCATCACACCATCC
ATCTGGAGGCCAACAGGCTGGCTGGCTCGAGCTCAGGAGGCCCTGAGGACTGCACACC
GGGCCAACACCTCCTGCCCTCCCTGGCATGTCCTGGGGAGGATTTGAGGGAGCT
CACTGCCTACCTGGCTGGGCTGTGCCCACACAGCAGTGCCTCTCCCTGAGTGCCTG
TGTAGCTGGGATGGGATTCTAGGGCAGATGAAGGACAAGGCCCACTGGAGTGGGTTTC
TTTGAGTGGGAGGCAGGGACGAGGAAGGAAAGTAACCTGACTCTCCAATAAAACCT
GTCCAACCTGTGAAA

FIGURE 100

MHGSCSFLMLLPLLLLVLATTGPVGALTDEEKRLMVELHNLYRAQVSPTASDMILHMRWDEE
LAAFAKAYARQCVWGHNKERGRRGENLFAITDEGMDVPLAMEEWHHEREHYNLSAATCSPGQ
MCGHYTQVVWAKTERIGCGSHFCEKLQGVVEETNIELLVCNYEPPGNVKGRPYQECTPCSQC
PSGYHCKNSLCEPIGSPEDAQDLFYLVTVEAPSFRATEASDSRKMGTPSSLATGIPAFLVTEV
SGSLATKALPAVETQAPTSLATKDPPSMATEAPPCVITTEVPSILAHSLPSLDEEPVTFPKS
THVPIPKSADKVTDKTKVPSRSPENSLDPKMSLTGARELLPHAQEEEAEEAELPPSEVLAS
VPPAQDKPGELQATLDHTGHSSKSLPNFPNTSATANATGGRALALQSSLPGAECPDKPSVV
SGLNNSGPGHVWGPLLGLLPLVLAGIF

Signal sequence:

amino acids 1-22

N-glycosylation site.

amino acids 114-118, 403-407, 409-413

Glycosaminoglycan attachment site.

amino acids 439-443

Casein kinase II phosphorylation site.

amino acids 29-33, 50-54, 156-160, 195-199, 202-206, 299-303

N-myristoylation site.

amino acids 123-129, 143-149, 152-158, 169-175, 180-186, 231-237,
250-256

Amidation site.

amino acids 82-86, 172-176

Peroxidases proximal heme-ligand signature.

amino acids 287-298

Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 1.

amino acids 127-138

Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 2.

amino acids 160-172

TOP SECRET//SI//REL TO USA, UK, FVEY

FIGURE 101

FIGURE 102

MVDVLLLFLSLLFHISRPDLSHNRLSFIKASSMSHQLQSREVKLNNNELETIPNLGPVSAN
ITLSSLAGNRIVEILPEHLKEFQSLETLDLSSNNISELQTAFFPALQLKYLYLNSNRVTSMEP
GYFDNLANTLLVULKLNRRNISAIAPPKMFPLQLQHLELNRRNKKNVDGLTFQGLGALKSLSKMP
QRNGVTKLMGAFWGLSNSMEILQLDHNNLTEITKGWLGYGLLMLQELHLSQNAINRISPAWE
FCQKLSELDITFNHLSRLDDSSFLGLSLLNTLHIGNNRRVSIADCAFRLGSSLKTLDDKNN
ISWTIEDMNGAFSGLDKLRLIILQGNRIRSITKKAFGLDALEHLDLSDNAIMSLQGNNAFSQ
MKKLLQQLHLNTSSLCLCDQLKWLQPQVAEENNFSQFVNACCAHPQLLKGRSIFAVSPDGFWCD
DFPKPQITVQFETQSAIKGSNLFSFICSAASSSDSPMTFAWKKDNELLHDAEMENYAHLRRAQG
GEVMEYTTILRLREVEFASEGKYQCVISNHFGSSYSVKAKLTVNMLPSFTKTPMDLTIRAGA
MARLECAAVGHFAPQIAWQKDDGGTDFPARERRMHVMPEDDVFFIVDVKIEDIGVYCTAQN
SACSIISANATLTVLETAPSFLRPLLDRTVTKGETAVLQCIAGGSPPPQLNWTKDDSPLVVTER
HFFAAGNGVIIAVVCCVVGTSLVVVVIIYHTRRNEDCSITNTDETNLPADIPSYLSQGTIAD
WATGVVIIAVVCCVVGTSLVVVVIIYHTRRNEDCSITNTDETNLPADIPSYLSQGTIAD
RQDGYVSSESGSHHQFVTSSGAGFFLPQHQDSSGTCHIDNSSEADVEAATDFLCPFLGSTGP
MLKGNVYGSDFETYHTGCSPPDPTVLMHYEPSYIKKKECYPCHSEESCRSFNSNISW
PSHVRKLLNTSYSHNEPGMKNLCLNKSSLDFSANPEPASVASSNSFMGTFGKALRRPHLDA
YSSFGQPSDCQPRAFYLAHKSSPDLDSGSEEDGKERTDFQEENHICTFKQTLENYRTPNFQS
YDLDT

Signal sequence:

amino acids 1-19

Transmembrane domain:

amino acids 746-765

N-glycosylation site.

amino acids 62-66, 96-100, 214-220, 382-386, 409-413, 455-459,
628-632, 669-673, 845-849, 927-931, 939-943, 956-960

Glycosaminoglycan attachment site.

amino acids 826-830

Casein kinase II phosphorylation site.

amino acids 17-21, 39-43, 120-124, 203-207, 254-258, 264-268,
314-318, 323-327, 347-351, 464-468, 548-552, 632-636, 649-653,
671-675, 739-743, 783-787, 803-807, 847-851, 943-947, 958-962,
1013-1017, 1019-1023, 1021-1025

Tyrosine kinase phosphorylation site.

amino acids 607-615

N-myristoylation site.

amino acids 179-185, 197-203, 320-326, 367-373, 453-459, 528-534,
612-618, 623-629, 714-720, 873-879

FIGURE 103

GGGGAGAGGAATTGACCATGTAAGGGAGCTTTTTGGGGGTGGCTGTTGGGTGCTTCGAAAGATG
AAGGATGCGAGACGAGCTTCCTGAAACCAAACTGGATAACCTGATTTGTGCAAGAGAGAAGGAAGAAC
GAAGCTTTCTGTGAGCCCTGGATCTAACACAATGCTATATGTGACACAGGGAGGATTCAAGAAGAA
TAACCCAGAGTAGACCCGGGGGGTGGTGTCTGACATAAATAATCTTAAAGCAGCTGTTCCCTCC
CCACCCCCAAAAGGATGTGAAAGTGAAGAACCGAGGATTCAAGAAGAAAAGTATGTTCATTTCTC
TAAAGGAGAACAGTGAACCCAGGAGATTTTGGGATGAAAGTGGGGCTTTTACTAAAGTAAAGAAGACT
GGTGTTGGTGTGTTCTCTTGGAAATTCACACAGGAGAGGAAATTAAATAATACATCTGAAAGAAA
TTTCAGAGAAGAAAAGTGGACCCGGAGATTGAGGATTGATTTGGGGAGAGAAAACAGAGACAGCTGGA
TTTGTGCTTATGTTGACTAAATGACGGATAATTGAGCTTCTCTTCAACCCCTGGATTCCATCTGGATGTTGCT
TTTATCTCTTGGATCAAGATCATGCTTCTCTTCTTCAACCCCTGGATTCCATCTGGATGTTGCT
GTGATCAGTCTGAAATACACTGTTGAATTCAGAGGACCAACACAGAGATAATTATGATGATGTTGACAAAGAT
GACCTTACATCCACAGAGATAATGAGTCTAGGTTAACAGGGCCATTATTGACCCCTGCTTGTGCT
GCTGGCTTCAACTCTGTGGTGGCTGGCTGGCTCAGACCTGCCCTCTGTGCTCTGCAAGAA
CCAGTTCAGCAAGGATTTGGTGTGGAAACCTCCGCTGGAGGTTGGCTGGAGATCCTCACCACACAGGCT
GCTGAACTCCATGAGAACCAATTCAGATCATCAAACTGCTAACGACTTGGGACTCTGGAAATCT
ACAGTTGAGTAGGACCATATCAGAGAACATTGGGAACTTCAACGTTCTGGGCAACTTCAACACTCTGGA
ACTCTTGACAACTCTTCAACTCATCCGGATGGAGCTTTTACTATGCTTAAACTGAAGGAGCTCTGGTT
GGCAACACCCCTGGAAAGCATCCTTCTATGCTTAAACAGAACTTCTTCTTGGCGGACTAGACATTAG
GGAATTGAAAGACTTCTCATACATCTCAGAGGCTTCTTGAAGGTTGGCTTCAACTTGGGAACTCTG
CATGTCACCCATCTGGGAATCCCTAACCTCACCCTCATAAAACACTGATGAGCTGGATCTTCTGGGAATCA
TTTACTCTCATGACCTTCTTCACTGATCATGAGGGCATACATTGAGGATGATACAGTCCAGAT
TCAACTGATTGAACCGGAACTGGCTTGAACCCCTTCACTGAGGAGATCAACCTTGCAACACAAATCTAAC
ATTACTGCTCATGACTCTGGCTCAGTGGTGGATAAAAGGACGGCCCTGGACACAGCTTGTGCCCCGGT
TAACACTCTCCCACTCTAAAGGGGGAGTACATTGGAGAGCTGACAGAAATTACTTCACATGCTATGCTCCGGT
GATGTTGGAGCCCCCTGAGACCTCATGTCAGTGGAGGAGCTGAGCTGAAATGTCGGGCTTCACACATC
CCTGACACATCTGATCTCTGGATTACTCTCAAACTGAGCTCATGACACATGAGCTGGGAGTGGCT
GCTCAGTGTGTTGACTTAAATTCACAAATGTAACTGTGCAAGAGATAACGGCATGTAACATGTTGAGTAA
TCCCTTGGGATACTACTGCTTCAGGCAACCCCTGAATTTACTGAGGAAACCAACTCTCCCTTCTTACT
AACCGTCACAGTAGAGACTATGGAACCGTCTCAGGATGAGGACGGGACACAGATAACAAATGTTGGGCTTCACTCC
AGTGGTCTGACTGGAGACCAACCTGACCCCTCTCACACACACAGAGGTCGACAGAGAAAACCTT
CACACATCCCAGTAGCTGATATAAAACAGTGGGACCTGGGAGATTGAGGAGCTGAGAGACTACAAATCTACAT
TGGGTTGGTGTGGCCATCACACTCATGGCTGGAGCTGATCTGGTCACTTCTACAAAGATGAGGAGACGACCCA
TCGGAAAACACATCACGGCCCAACAGGACTGTGAAGAATTATTAAATGTGAGATGAGATTTACGGGAGACACCC
CATGGAAGGCCACTGGCCATGAGCATGAGCACCTAAATCAACTGAGCTGAGTGAACCGTTATTGATCCGAATGAA
CTCTAACAGACATGTACAGAGACTCAAATCTAAACACTGAGCTGAGTCAAAAGAACAAATCAACAAAAAA
GACACTTATTAAAGACACAAATGACTGGCTAAATCTACTGTTCAAAAGGAGTCTTTTACAAAAAA
AAAAGAAAAGAAATTATTAAATCTATTGTGATCTAAAGCAGACAAAAAA

FIGURE 104

MLNKMTLHPQQIMIGPRFNRALFDPLLVLLALQLLVVAGLVRAQTCPSVSCSNQFSKVIC
VRKNLREVPDGISTNTRLLNLHENQIQIIVKVNFSKHLRHLIELQLSRNHIRTIEIGAFNGLA
NLNTLELFDNRLTTIPNGAFVYLSKLKEWLWRNNPIESIPSYAFNRIPSLRRLDGELKRLS
YISEGAFEGLSNLRYLNLAMCNLREIPNLTPLIKLDELDLSGNHLSAIRPGSFQGLMHLQKL
WMIQSQIQVIERNAFDNLQSLVEINLAHNNLTLPHDLFPLHHLERIHLHHNPWNNCNDIL
WLSWWIKDMAPSNTACCACRNTPPNLKGRYIGELDQNYFTCYAPVIVEPPADLNVTGMAAE
LKCRASTSLSLTSVSWITPNGTVMTHGAYKVRIAVLSDGTLNFTNVTQDGTGMYTCMVNSVGN
TTASATLNVTAATTPFSYFSTVTVETMEPSQDEARTTDNNVGPTPVVDWETTNVTTSLTPQ
STRSTEKTFTIPVTDINSGIPGIDEVMTKTIIGCFVAITLMAAVMLVIFYKMRKQHHRQN
HHAPTRTVEIINVDDIEITGDTPMESHLPMPAIEHEHLNHNSYKSPFNHTTVNTINSIHSS
VHEPLLIRMNSKDNVQETQI

Signal sequence:

amino acids 1-44

Transmembrane domain:

amino acids 523-543

N-glycosylation site.

amino acids 278-282, 364-368, 390-394, 412-416, 415-419, 434-438,
442-446, 488-492, 606-610

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 183-187

Casein kinase II phosphorylation site.

amino acids 268-272, 417-421, 465-469, 579-583, 620-624

N-myristoylation site.

amino acids 40-46, 73-79, 118-124, 191-197, 228-234, 237-243,
391-397, 422-428, 433-439, 531-537

FIGURE 105

FIGURE 106

MSAPSLRARAAGLGLLLCAVLGRAGRSDSGGRGELQPSGVAEARPCPTTCRCLGDLDDCSR
KRLARLPEPLPSWVARLDLSHNRLSFIKASSMSHLQSLREVKLNNNELETIPNLGPVANSNIT
LLSLAGNRIVEILFEHLKEFQSLETLDLSSNNISELQTAFPALQLKLYLNSNRVTSMEPGY
FDNLANTLLVLKLNRNRISAIAPPKMFKLPQHQHLELRNPKINVDGLTFQGLGALKSLKMQR
NGVTKLMDGAFWGLSNSMELQLDHNNLTEITKGWLGYGLLMLQELHLSQNAIRISPDAWFC
QKLSELDDLTTFNHLSSLRDDDSSFLGLSLLNLTIHIGNNRVSYIADCAFRGLSSLKTLSDLKNNEIS
WTIEMNGAFSGLDKLRLLIQGNRISITKKAFTGLDALEHLDLSDNAIMSLQGNAFSQMK
KLQQLHLNTSSLLCDCQLKWLQWVAENNNFQSFSVNAASCAPQQLLKGRSIAVSPDGFCDF
PKPQITVQPETQSAIKGSNLSFICSAASSSDSPMTFAWKDNEELLHDAEMENYAHLRAQGE
VMEYTTILRRLREVEFASEGKYCVISNHFGSSYSVKAKLTVNMLPSFTKTPMDLTIRAGAMA
RLECAAVGHPAPQIAWQKDGGTDFPAARERRMHVMPEDDVFFIVDVKIEDIGVYSCTAQNSA
GSISANATLTVLETPSFLPLDRRTVKGETAVLQCIAGGSPPPKLNWTKDSDPLVVTERFH
FAAGQNLLIIVDSDVSDAKYTCMSNTLCTERGNVRLSVPPTPTCDSPQMGTAPSLLDDGWA
TVGVVIIAVVCCVVGTSLVVVVIYHTRRRNEDCSITNTIDETNLPADIPSYLSSQGTLLADRO
LKGVVYSGSDPFETYHTGCSPPDRTVLMHDYEPSYIKKKECYPCHPSEESCRSFSNISWPS
HVRKLLNTSYSNHEGPGMKNLCLNKSSLDPSANPEPASVASSNSFMGTFGKALRRPHLDAYS
SFGQPSDCQPRAFYLKAHSSPDLDSGSEEDGKERTDFQEEHICTFKQTLNEYRTPNFQSYDLDT

Signal sequence:

amino acids 1-27

Transmembrane domain:

amino acids 808-828

N-glycosylation site.

amino acids 122-126, 156-160, 274-278, 442-446, 469-473, 515-519, 688-692, 729-733, 905-909, 987-991, 999-1003, 1016-1020

Glycosaminoglycan attachment site.

amino acids 886-890

Casein kinase II phosphorylation site.

amino acids 99-103, 180-184, 263-267, 314-318, 324-328, 374-378, 383-387, 407-411, 524-528, 608-612, 692-696, 709-713, 731-735, 799-803, 843-847, 863-867, 907-911, 1003-1007, 1018-1022, 1073-1077, 1079-1083, 1081-1085

Tyrosine kinase phosphorylation site.

amino acids 667-675

N-myristylation site.

amino acids 14-20, 36-42, 239-245, 257-263, 380-386, 427-433, 513-519, 588-594, 672-678, 683-687, 774-780, 933-939

Leucine zipper pattern.

amino acids 58-80, 65-87

FIGURE 107

CAAACATTGCGTCGGGAGGCGCCAGCTTGACTTGAATGGAGGGAGCCGAGCCGGAGCGCAGCTGAGAC
TGGGGAGCGCTTCGGCTGTGGCGCGCTGGGCCGGCGCAGCAGGGAGGGAGCTGTGCTTCG
CTGCTCCACGAGGCCACTGGTGTGAAACGGGAGAGCCCTGGTGGTCCCGTCCCTATCCCTCTTATA
GAAACCTTCAACTGGAAAGCTTGGAGGGGAGCTGAGCAAGGGAGGGCTGATGGTGAAGGAGGGCGGCTGATCTGAG
GCGCACAGCATTCGGAGTTACAGATTTACAGATAACCAAAATGGAGGGAGGAGGAGACAGCCCTGCTGGT
TCCATCAGCCCTGGGCCAGGGCATCTGACTCGGACCCCTGGAGGGCACCCTGGCAGAGCCGGCTGAGGAGCTGGCTGC
TGCCTCTGCTGCTGCGGCCACAGCTGACCTGGGACCTGTGCTTGGCCCTGAGGGCCAGGATTTGGCGAA
GTGGGGCCACAGCTGAGCCCCAGAGAGAACGAATTGGCGAGGAGGGCTGCTGGTACTGAGCCCTGAGG
AGCCCCGGCTGGCCAGCGGGCTAGCTGGCTGTTCCGGGACACTGGCTGAGCACCAACCAACCTATCTGAGAACACAGC
GGGTATTGACCTGGTGAAGTCTCCGGGACCTGGCTGAGCACACCAACCTATCTGAGAACACAGC
TGGAAAAGATCTTGGAGGACTCTCCGGCTGAGCACCGGAAACTCTGAGAACACTGAAACCTGCAAAA
CTTGGCGAGGGTCCAGAGAACGGCTTGGACCATCTGACCAACTTCAATTACTGTACTTGGCAAATACAGC
TGACCTGGCACCCGCTCTGGCCTGAAACGGCTGATCAGTGTGGACTTGTGCTCCAACATCTACCAAGATCT
ATGGCTCACCCTTGGCCAGAACGAAACTTGGAGGTTGTGACTCTGGCCTGAAACAAACAGCTGGCAGAGCCGGC
TGGCCGAACACATGTGCTGACGCTTGGCACAACTGGGCTTGTGCTTGGCCTGAGCAACTTCTGGCCACCTGC
CCAACGACTTGGCCCTGACCTGAACTGGCCTGAAACAAACAGCTGGAGAACGATCCCCCGGGGCT
TCAGGAGACTGGAGCCTGGCGAGTATACCTGGAGAACACACTTGGACTGAGCAGGGCTGGAGAACAGA
CCTTGTGAGCTCTGGCCTGGAGACTCTGGATCTGGTCAACGGGACTTGGGCTGAGAACACTTGGCTG
GGCGAGGCTGTGCTGCTGCACTTGGAGAACAGCCATCCGGAGGCTGGAGCGGAATCTGGCTGACCCCCATCC
GCACCTGGAGTACCTGGCTGCTGACGCAACAGCTGGCGGAGGGCATTCACCCACTGGCTTCCAGGGC
TCAAGCGTTGACCTGACGGGACCTGTAAACAAACGGCTGGAGGCGGTGCGCTGGCTGGCCCTGGCGCTGC
GCACCCCTATGATCTGGCACACAGGATCACAGGATTGGCCGGAAAGACTTGGCCACCACTTCTGGAGG
AGCTAACCTCAGTACACCCGATCACAGGCCAACGGTGCACAGCTGGCAGCCCTTCCGAAGCTGGCTG
GCTGCTGGAGCTGTGGGCAACGGGCTGACAGCTGGCCTGGGCTGCGCTGGAGGATCTGGCTG
TCAAGCGGAATGAGCTGGCTGGCTTGGAGGGCTGGCGGAGGCTGGCTGAGCTGGCTGAGGAG
CCACCAAGGGACTGGCGAGGGCTGGCCCTGGGCTGGCGACTGGCTGAGCTGGCTGAGGAG
TCGCGGGAAATCAGCTCACAGGATCTGGGGCTGGGGCTGGGGACTTGGAGTACCTGTACCTGGAGAACACA
AGATAGTGGCTGGTGGCCGGAAATGGCTTCTGACTCTGGCAGGCCCACCTCAAGGGATCTTCTCAGGTTAAACAGC
TGGCTGGGGCTGGGGAGACTGGCTGGGGCTGGGGCTGGGGAGGAAAGAGGAGGAGGAGGAGGAGGAGGAGG
TAGAGTTGGTGACATTCAAGGAGCGTGGCGCTTGGGGAGGAAAGAGGAGGAGGAGGAGGAGGAGGAGG
AGGAAGAGGAAACAGAATTAGTGAACAGGTGATGCAAGTGTGACTTAGATGATGAGCAGGGGACTCTTTCTGC
AGCACACGCCCTGTGCTGTGAGCCCCACTGGCTGCTCACACAGCACACCCAGCTGACACATGAGGCA
TCCACACATGACAGGGCTGACACAGCTCATATCCACCCACCCCTTCCACGGCGTGTCCACGGCAGAACATG
ACACACATCACACCTTCAACACCCAGCTGAGCCACACAAACTACCCCTAACACAGCTGACACATGAGGCA
CCCCACTACCGCTGCCACGCCCTGAAATCATGAGGGAGGGTCTGCCCTGGCACACACAGGCCACCA
TTCCCTCCCGCTGCTGACATGTGATGCTGCTGATGCAACACACACACACACAGCTGACAGGGAA
CAGGGCTCCAAGGCTATGGCCACAGCACGCTCTGGCCAGGAGATCAGGATAGCTGGCTGAGGAGGAG
GGCATCTGTGCTGGCTGGCTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG
GGAACTCACAAAAGCTGGCTTATTCTCTTCCCATCTATGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGG
TGGCCACCCCTGCTCTCAGGTGCTGGGAGCTGACTCTGGCTAAGAGTCCCTGGCCAGGCCCTGGCAGGACA
CAGGCCACTTCAATGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG
CAGGAGTGAAGCAGAGGTGATGGGGCTGGGCTGAGCCAGGGAGGAGGAGGAGGAGGAGGAGGAGGAGG
GTTCTCAGGCTGTGGGGAGGTTCCGGGTGCCCTTATTCTTTCTAAGGAAAAAAATGATAAA
CTAAAGCTGATTTCTGGTATAGAAAAACTAATATAAAAGCATTATCCCTATCCCTGCAAAAAAA

FIGURE 108

MEGEEAEQPAWFHQWPWRPGASDSAPPAGTMAQSRLVLLLLLLPPQLHLGPVLAVRAPGFGRS
GGHSLSPPEENEFEEEPVLVLSPEEPGPAAVSCPRDCACSGEGVDCGGIDLREFPGDLP
EHTNHLSLQNNQLEKIYPEELSRLHRLETLNQNNRLTSRGLPEKAFAEHTNLNYLYLANNK
LTLAPRFLPNALISVDFAAANYLTAKIYGLTFGQKPNLRSVYLHNNKLADAGLPDNMFNGSSNV
EVILILSSNFLRHVPKHLPPALYKLHLKNNKLEKIPPGAFSELSSLRELYLQNNYLTDEGLDN
ETFWKWLSSLEYLDLSSNNLSRVPAAGLPRSLVLLHLEKNAIRSVDANVLPIRSLEYLLHSN
QLREQGIHPLAFQGLKRLHTVHLYNNALERPVPSGLPRRVRTLMILHNQITGIGREDFATTYF
LEELNLSYNRITSPQVHVDRAFRKLRLRSLDLSGNRLHTLPPGLPRNVHVLKVKRNEAALA
RGALAGMAQLRELYLTSNRLRSRALGPRAWDLAHLQLLDIAGNQLTEIPEGLPESLEYLYL
QNNKISAVPANAFDSTPNLKGIFLRFNKLAVGSVVDSAFLRLKHLQVLDIEGNLEFGDISKD
RGRLGKEKEEEEEEEEEEETTR

Signal sequence:

amino acids 1-48

N-glycosylation site.

amino acids 243-247, 310-314, 328-332, 439-443

Casein kinase II phosphorylation site.

amino acids 68-72, 84-88, 246-250, 292-296, 317-321, 591-595

N-myristoylation site.

amino acids 19-25, 107-113, 213-219, 217-223, 236-242, 335-341,
477-483, 498-502, 539-545, 548-554

Leucine zipper pattern.

amino acids 116-138, 251-273, 258-280, 322-344, 464-486, 471-493,
535-557

FIGURE 109

GGGAGGGGGCTCGGGCGCGCGAGCAGACCTGCTCCGGCGCCCTCGCGCTGTCTCCGGGAGCG
CAGTAGCCGGGGCGAGGGCTGGGGTTCTCGAGACTCTCGAGGGGCCCTCCCATCGCGGCCACACCC
CAACCTGTCTCGCGCCACTCGCTCGGCCCAAGGACCGCTGCCAACATGATTCTCCCTGGCGCTGGT
GCTGGTATGCTCGCTACTCGAGGGGCCCGAGCTGACGGGAGGTGGCCAGGCAAATAGTGTCACTGAT
TGGCTATGCTGTTAGGGAGGACTGACTCTGCTGGGGCTGGCCAGTCTGGGGAGCTGTCACTG
TGTGCTGGCCAAACGAGTGCACAAACATGGTGAATGTATCGGGCCAAACAGTCTCAACTGTCATCTGGTTATGGCTGG
AAAAACCTGTAATCAAGATCTAAATGAGTGTGGCTGAAGCCCGCCCTGTAACCAAGGTGCTGAACACTTA
CGCGAGCTACAAGTGTACTGCTCAACGGATATATGCTCGCCGATGGTCTCTGCTCAAGTGCCTGACCTG
CTCATGGCAAACCTGTCAGTATGGCTGTGATGTGTTAAAGGCAAATCTCGGTGCCAGTGCCTGGCT
GCACCTGGCTCTGTGATGGGAGACCTGTGATGATGAATGTGCTACAGGAAGACGCTCTGCCCTAGATT
TAGGAATCTGTCAACACTGGGAGCTACATCGCAAGTGTATAAGGCTTCGATCTCATGTTATGGGAG
CAAATTAATCATGTCACTGACATAGCAGCTCACTTGTGCACTGATCAGTCAGCAGCTTGTCTGATGTATAA
CGTAGCTGGCTCAACAGTGCACAAATGTAAGAAGGATACAGGGTGACTGACTGTGTGTTATGCCAA
AGTTATGTTGAACTTCAGGTCATTCATGTCACAGTACCAAAAGGAAATGTCACCTTTAAAGGGTGACACAGGAA
TAATAATTGGATCTCTGATGTTGGAAAGTACTTGTGGCTCGGAAGACACATATCTCTCTATCATACCA
CAGGCCACTCTAAGCACAACAAAGCCTACACCAAAAGGCCAACACAACTCCACTCACCACCCAGGAA
CTTGGCCAAAGACGCTCAAGACACCTTCAACCCCAAGGCAACACCCAGGACTGCAACATATAGC
ACACCTGGCAGTACACCTCCAGGGGAGTACAGTGCACAAAGGGTACAGACAGACCCCTCAGAACACCCAGG
AGATGTGTCAGTGTCTGGTACACAGTGTGTTAACTTGTGACATGGACTTGTGATGCTACGGGAGAA
TGACTTGTGACTGGAAACATCAGGGACCCAGCAGGGTGCACATCTGACAGTGTGGCAGCCAAGGCCAG
GGGAAAGCTGCGACCTGGTGTACTCTCGGCCGCTCATGCTTCACTGGGGACCTGTGCTGTCAATTAGGCA
CAAGGTGGGGCTGCACTCTGGCACACTTCAACGGTGTGAGAAAACAGGGTGCACAGGAGCAGCCCTGTG
GGGAAGAAGATGGTGGCCATGGCTGGAGGCAAACAGATCACCTTGGCGAGGGCTGACATCAAGAGGAA
AGATGATTAAAGGTTGGAAAAGAATCTATGTTAAAGGAAACTGGGATTATTGAGCCTGGGAG
AGAGACTGAGGGCAAACCATGTATGGTTTCAAGATATGAGGGTGGCACAGAGGGTGGGACCTG
TTCTCCATATGCACTAAAGAATAGAACAGAGGAACACTGGCTAGACTGACTATAAGGGAGCATTTCTGGCAGG
GCCATTGTGATGAAACTTCATAAAAAAAGTGTGAAATCTCAGTATCTCTCTCTCTTAAAGGTTAGA
TAAAATTTGTCTATTAAAGATGTTAAAGATGTTCTTACCCAAAGGAAAGTAAACAAATTAAGAATTTCCAAA
AGATTTTGATCTACTAGTGTACTGATGTCAGTAAAGTAACTTTAGAATAAATTTGGACAAGGCTTAATTAGG
CATTTCCCTCTTGACCTCTTAATGGAGGGATTGAAAGGGAAAGGCCACCAATGCTGAGCTACTGAAATA
TCTCTCCCTATGGCAATCTGCACTGTTAAAGGAAACTTATTCTCCAAATGAGAGTATGATGGAC
AGATATTAGTATCTGCACTGTTACTGCTGTTCTGGCTGTTTCAATGTTCTCATGGTAAAGGTTAAAGGTTAAAGC
TTCTTCTTCAATGGATGATGTTAGTTTTTTAAAGGATCTTCAAGGAACACAGTTCAAGAG
ATTTCATGGGTGCAATTCTCTGCTCTGCTGTGACAAGTTATCTGGCTGCTGAGAAAAGAGTGCCTGGCC
ACACCGGAGACCTTCTCITCACCTCATGAGTGTACTGCTGTTCTCTTATCAATTGGACTCTCCAGGTTCCAC
AGAACAGTAAATTTTGAACATAGGCTACAATAGAGGTCTTCTGCTGCTTAACTCTGGTAAAGGGAGGCTGG
AGGGGAAAATAATCATTAAGCTTGTGACTAACGGAGAATATGCTGATGATCATTTTAATGGTCTATT
TCTTATGGTATGATTAACCTGACACGCTGAAGATGAAAGGGAAAATAATGAAAATTTTACTTTCTGATGGCAA
TGATACATTGCACTAAACTGATGAGGAAGTTACCAAAAGTACTGATTAACATCTGTTTATTATTAATGTTT
CTAAAAAAATGTTAGTGGTTTCCAAATGGCTAATAAAAACAAATTATGTAATAAAAACACTGTTAGTAAT

FIGURE 110

MDFLLALVLVSSLYLQAAAEEFDGRWRPRQIVSSIGLCRYGGRIDCCWGWARQSWGQCQPVQCQPRCKHGE
CKHGE CIGPNKCKCHPGYAGKTCNQDLNECGLKPRPCKHRCMNTYGSYKCYCLNGYMLMPDGSCSSALTCS
MANCQYGDVVKGQIRCQCPSPGLHLAPDGRITCVDVDECATGRASCPFRQC
VNTFGSYICKCHKGFDLMLYIGGKYQCHDIDECSLQYQCSSFARCYNVRGSYKCKCEGYQGDGLT
CVCYIPKVMIEPSGPIHVPKGNGTILKDTGNNNNWIPDVGSTWPPKTPYIPPIITNRP
TSKPTTRPTPKPTPIPTPPPPPPLPTELRTPLPPTTPERPTTGLTTIAPA
ASTPPGGITVDN RVQTDPPQKPRGDVFSVLVHSCNFHGLCGWIREKDNDLHWEPIRD
PAGGQYLTVSAAKAPGG KAARLVLPLGRLMHSGDLCLSFRHKVTGLHSGTLQVFVRKHGAHGA
ALWGRNGGGHGRQTQITLRGADIKSESQR

Signal sequence:

amino acids 1-17

N-glycosylation site.

amino acids 273-277

Casein kinase II phosphorylation site.

amino acids 166-170, 345-349

Tyrosine kinase phosphorylation site.

amino acids 199-206

N-myristoylation site.

amino acids 109-115, 125-131, 147-153, 191-197, 221-227, 236-242,
421-427, 433-439, 462-468, 476-482

Aspartic acid and asparagine hydroxylation site.

amino acids 104-116, 186-198, 231-243

Cell attachment sequence.

amino acids 382-385

EGF-like domain cysteine pattern signature.

amino acids 75-87

090902613 - 0710901

FIGURE 111

CTCTTTGAAAGGATTATCACCTGATCAGGTTCTCTGCATTGGCCCTTAGATTGTGA
AATGTGGCTCAAGGCTTCACAACTTCTTCTTCTTGCACAGGTGCTTCTGGGGCTGA
AGGTGACAGTGCATCACACACTGTCCATGGCTCAGGGTCAAGGGCTTACCTACCCG
CATACTGGCTTCAACACTTCAGCATCAGAACATCAGATCATGGCTATTGGAGAGACCCA
ACAATGCCCAAATACTTACTGGGCTCTGTGAATAAGTCTGTGGTCTGTGAGTGAATACC
AACACAATGTCACCATGATGCCACCCAAATGCATCTGTCTTACACCCACTGCAAGTTCCT
GTGAAAGGCAATTACATCGTGAAGGTCAACATTCAAGGAAATGGAACTCTATGCGAGCTCA
GAAGATAACAGTCAGCTGTGATGATCTGTCAACAAAGCAGTGGTCGAGATTCTATCCCT
CTGGGGCTGTGGAGTATGGGGAAACATGACCTGTACATGCCATGTGAAAGGGGCACTCGG
CTAGCTTACAATGGCTAAAAATGGGAGACCTGTCCACACAGCTCCACTACTCTTTTC
TCCCCAAAACAAATACCTCTATATGCTCAGTAAACAGGAAGACATGGGAAATTACAGCT
GCCTGGTAGGAACCTGTCAGTGAATGGAAAGTGTATCATATTGCCCCATCATATTAT
GGACCTTATGGACTTCAAGTGAATTCTGATAAAGGGCTAAAGTAGGGGAAGTGTCTACTGT
TGACCTTGGAGGAGGCCATCTTGTGATTTCTGTGATTCTCATCCCCAACACCTACT
CTGGATTAGGGAGGACTGACAATACATATATCATTAAGCTGGGCTCTGTTAGGTT
GCATCTGAGAAAGTAGCCAGAAGACAATGGACTATGTGCTGTGTTACAACACATAAC
CGCGCAGGCAAGTAAACTCATTCACAGTTATCATCACTTCCGTAGGACTGTGAGAACCTG
CACAGAAAGGAAAATCATGTCACCTTCTAGCAAGTATACTGGAAATCATATTGTTG
ATATCCATGTGCTTCTCTTCTATGGAAAAAAATCATACCCCTACAAAGTTATAAAACAGAA
ACTAGAAGGCAGGCCAGAACAGAACATACAGGAAAGCTAAACATTTCAGGCCATGAAGATG
CTCTGGATGACTTCCGAATATATGAATTGTTCTGTCTTCCAGATGTTCTGTGTTCCAGG
ATTCCAACAGGCTGTCTTCCAGGCTCTGATTGTGATCTGGGAAAGATTGCAAGTACAGT
GTATGAAGTTTACGCACATCCCTGCCAGCAGAACATCTCAGAGTGAACATTCTGTGG
GCTAAACAGTACATTGAGTGAATTCTGAGAACATTTAAGGAAAAACAGTGAAAAGT
ATATAATCTGGAAATCAGTGAAGAACACAGGACCAACCTTCACTCATTTCTTACA
TGCAAGAACAGGCTTATGCAATTGAACTGCAAGGTTCTCAGCATACACATGTCTT
GTGCAACAGAAAACATGGGGAAATATTCCCTCAGTGGAGACTGCTTCTGTGAGCAGG
GGAGAACGAAAGTGACAGGGTTCTCATAAAGTTGTGATGAAATATCTACAAACCTCA
ATTAGTTCTACTCTACATTCTACATCATCACACACTGAGACATCTGTCTCACCACAAA
TTGGGAAACTTCTACATTGTCAGGACTTCTGTGTTTATTAATTTTTATAGTGT
TTAAGAATGCTAAATTATGTTCAATTTCAGGAACTTCTACATCTGTGTTATTGTGAA
CAAAGTAATTAAGGAGTGGTGTCAACAAAACAAAATCTGCTTCTCTTCTTCAATCACC
AGTAGTATTGAGAAGACTTGTGAAACTTAAAGGAAATGACTTAAAGTCTTATTTT
TTTTTCAAGGAAAAGTGAATCAAATAATTATCTGTTTTGCTTGTGTTT
AAAAAAAAAAAAAA

FIGURE 112

MWLKVFTTFLSFATGACSGLKVTPSHTVHGVRGQALYLPVHGFHTPASDIQIWIWLFRPH
TMPKYLLGSVNVKSVPDLLEYQHKFTMMPNPNASLLINPLQFPDEGNYIVKVNIQGNGLTSLASQ
KIQVTVDDPVTKPVQIHPPSGAEVYVGNMTLTCHVEGGTRLAYQWLKNGRPVHTSSTYSFS
PQNNTLHIAPIVTKEDIGNYSCLVRNPVSEMEDSIIMPIIYGGPYGLQVNSDKGLKVGEVFTV
DLGEAILFDPCSADSHPPNTYSWIRRTDNTTYIIKHGPRLLEVASEKVAQKTMVDYVCCAYNNIT
GRQDETHFTVIITSVGLEKLAQKGKSLSPASITGISLFLIIISMCLLFLWKKYQPYKVIKQK
LEGRPETEYRKAAQTFSGHEDALDDFGIYEFVAFPDVSGVSRIPSRSVPASDCVSGQDLHSTV
YEVIOHIAPOODHPE

卷之三

Signal sequence:

amino acids 1-18

Transmembrane domain:

amino acids 341-359

N-glycosylation site.

amino acids 73-77, 92-96, 117-121, 153-157, 189-193, 204-208, 276-280, 308-312

Casein kinase II phosphorylation site.

amino acids 129-133, 198-202, 214-218, 388-392, 426-430, 433-437

Tyrosine kinase phosphorylation site

amino acids 273-280

N-myristoylation site.

amino acids 15-21, 19-25, 118-124, 163-167, 203-209, 231-237, 239-245

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 7-18

FIGURE 113

FIGURE 114

MAPSGSLAVPLAVLVLLWGAPEWTHGRRSNVRVITDENWRELLEGDMIEFYAPWCPCACQNL
QPEWESFAEWGEDLEVNIAKVDTEQPGLSGRFIITALPTIYHCKDGEFRYYQGPRTKDFI
NFISDKEWKSIEPVSSWFGPGSVLMSSMSALFQLSMWIRTCHNYFIEDLGLPVWGSYTVFAL
ATLFSGLLGLCMIFVADCLCPSKRRRPOPYPYPSKLLSEAQPLKKVEEEQEADEEDVSE
EEAESKEGTNKDFPONAIRORSLGPSPLATDKS

Signal sequence:

amino acids 1-26

Transmembrane domain:

amino acids 182-201

Casein kinase II phosphorylation site

amino acids 68-72, 119-123, 128-132, 247-251, 253-261

Tyrosine kinase phosphorylation site

amino acids 107-115

N-myristoylation site

amino acids 30-36 183-188

Amidation site

amino acids 25-29

FIGURE 115

CGAGTGTCCAGCTGCGGAGACCGTGTATAATTCTGTTAACTAATTCAACAAACGGGACCCCTT
CTGTGTGCCAGAAAACCGCAAGCAGTGTCAACCCAGTGGACAGGGGAGTTGGAAGAGCCTG
AAGGTCTCGGCCAGACAGCAGTGTGACACTCCCTCTGTGACCAATGAAACTCTGGGTGCTGC
ATGCTGATGCCCTGGTTGGTCTGTGAGCTGTGTCAGGCCGAATTCTCACCTCTATTG
GGCACATGACTGACCTGATTATGAGAGAAGAGCTGGCAGTCTGAAAGACTACATC
CTTGTGGAGGAAGCCAAGCTTCAAGATAAGAGCTGGGCAACAAAATGGAAGGCCCTGGAC
TAGCAAGTCAGCTGCTGATGTCAGGGCTACCTGGCTCACCCCTGTGAATGCCCTACAAACTGG
TGAAGCGGCTAAACACAGACTGGCTGCGCTGGAGGACCTTGTCTGAGGACTCAGCTGCA
GGTTTATGCCAACCTCTGTGAGCGCAGTGTGAGGAGGAGATAGG
AGCTGCCAACGCCCTGTAGAGACTTCAAGGACACATACAGGCTGGACCCAGGCCAATTCTCA
GAGGGGAACCTCCAGGAACCAAGTACCAAGGAATGCTGAGTGTGGATGACTGCTTGGGATG
GCCGCTCGGCTAACATGAGGGACTATTATCATACGGTGTGATGGAGCAGGTGCT
AAAGCAGCTTGTGATGCCGGGGAGGGAGGCCAACAAAGGACAGGTGCTGGACTACCTCA
GCTATGCTGCTCCAGTTGGGTGATCTGCACCGTGCCCTGGAGGCTACCCGCCCTGCTC
TCCCTTGACCCAAAGCAGACAGCTGGAGGAATCTGGGTACTTTGAGCAGTTATTGGA
GGAAGAGAGAGAAAACGTTAACAAATCAGACAGAAGCTGAGCTAGCAACCCCCAGAAGCA
TCTATGAGAGGGCTGTGACTACCTGCTGAGAGGGATGTTACAGAGGCCCTCTGCTGG
GAGGGTGTCAAACGTACACCCCGTAGACAGAAAGAGGCTTCTGTAGGTACCACTGGCAA
CAGGGGCCACAGCTGCTCATGGCTTCTCAAAGGAGGGAGCAGTGGGACGCCCGCACA
TCGGTCAAGGTACTACGATGTCATGTCATGAGGAAATCGAGAGGATCAAGGAGATCGCAAA
CCTAAACTTGACGAGCCACCGTCTGTGATCCCAAGCAGGAGTCTCACTGTGCCAGCTA
CCGGGTTCCAAAAGCTCTGGTAGAGGAAGATGATGACCCCTGTGTGGCCCGAGTAATC
GTCGGATGAGCATATCACAGGGTAAACAGTAAAGACTTGAGAATTGTTACAGGTTGCAAT
TATGGAGTGGGAGGACAGTATGAAACGCCACTTCGACTTCTCTAGGGCACCTTTGACAGCG
CCTAAACAGAGGGAAATAGTTAGCGACGTTCTTAACATGAGTGTAGAAGCTG
GTGGTGCCACCGCTTCCCTGATCTGGGGCTGCAATTGGCTTAAGAAGGGTACAGCTGTG
TTCTGTTACAACCTCTGGAGCGGGGAAGGTGACTACCGAACAAAGACATGCTGCCCTGCC
TGTGTTGTGGCTGCAAGTGGGCTCCAAATAAGTGTCCATGACAGAGGACAGGAGTTCT
TGAGACCTTGTGGATCAACAGAAGGTTGACTGACATCCTTTCTGCTCTCCCTTCTGGTC
CTTCAGCCCCATGTCACACGTGACAGACACCTTGTATGTTCTTGTATGTTCTTATCAGGCT
GATTTTGGAGAAATGAATGTTGTCAGGAGCAGGGAGGACCATACTAGGGCAGCTCTGT
GTGACTGAAAGTCCCAGGCCCTCCATTGACCTGTGCTAGGCCATCCCTGGCCCAAGGCTAGGATCA
AAGTGGCTGAGCAGAGGTTAGCTGTAGCGCCTAGCAAGGTGCTTGTACCTCAGGTGTT
TTAGGTGTGAGATGTTCTGAGACCAAAAGTCTGATACCTGTTACATGTTGTTTTAT
GGCATTCTATCTATTGTGGCTTACCAAAAAATGCTCCCTACCAAGAAAAAA

FIGURE 116

MKLWVSAALLMAWFGVLSCVQAEFFTSIGHMTDLIYAEKELVQSLKEYILVVEAKLSKIKSWAN
NKMEATLTSKSAADAEGLAHVPNAYKLVKLRLNTDWPALEDLVLQDSAAFGIANLSTVQRQFFP
TDEDEIGAAKALMRLQDTRYLDPGTISRGELPGTKYQAMLSVDDCFGMGRSAYNEGDYVHTV
LWMEQVQLKQLDAGEEATTKSQVLQDLYSAYVFQLGDLHRALELTTRRLLSLDPHSHERAGGNLR
YFEQLLEEEEREKTLTNQTEAELATPEGIYERPVDPYLPERDVYESLRCRGEVKLTPRQRKLF
CRYHHGNRAPQLLIAFPKEEDEWDSPHIVRYYDVMSEEEIERIKEIAKPKLARATVRDPKTG
VLTVASYRVSXSKSWLEEDDPVVARVNRNRMQHITGLTVKTAELLQVANYVGGGQYEPHDFDS
RRPFDGLKTEGNNRATFLFVNMSDVEAGGATVFPDLGAAIWPKKGTAVFWYNLLRSGEGDYR
TRHAACPVLVGCKWVSNKWFHERGQFRLPCGSTEV

Signal sequence:

amino acids 1-17

N-glycosylation site.

amino acids 115-119, 264-268

Glycosaminoglycan attachment site.

amino acids 490-494

cAMP- and cGMP-dependent protein kinase phosphorylation sites

amino acids 477-481

Casein kinase II phosphorylation site

amino acids 43-47, 72-76, 125-129, 151-155, 165-169, 266-270, 346-350, 365-369, 385-389, 457-461, 530-534

Tyrosine kinase phosphorylation site

amino acids 71-80: 489-496

N-myristoylation site

amino acids 14-30 131-137 171-177 446-452

Prokaryotic membrane lipoprotein-lipid attachment site

amino acids 8-18

Louise zipper pattern

amino acids 213-225

FIGURE 117

FIGURE 118

MRLSSLLALLRPALPLILGLSLGCSLSLLRVSWIQGECEGDPVCVEAVGERGGPQNPDSRARLD
QSDEDFKPRIVPYYRDPNPKYKKVLRTRYIQTGSRERLLVAVLTSRATLSTLAVAVNRTV
AHHFPRLLYFTGQRGARAPAGMQVVSQHGDERPAWLMSETLRHLHHTHFGADYDWFFIMQDDTY
VQAPRLAALAGHLSINQDLYLGRAAEFIGAGEQARYCHGGFGYLLRSLLLRLRPHLDGCRG
DILSARPDEWLGRCLIDSGLVGCVSQHOCQOYRSFELAKNRDPEKEGSSAFLSAFAVHPVSE
GTLMYRLHKRFSALELERAYSBIEQLQAQIRNLTVLTPEAGEAGLSWPVGLPAPFTPHSRFEV
LGWDYFTEQHTFSCADGAPKCPQGASRADVGADETALEQLNRRYQPRRLRFQKQRLLNGYR
RFDPARGMETYTL DLLECVTQRGHRRALARRVSLLRPLSRVEILPMPYVTEATRVQLVPLLL
VAEAAAAPAFLEAFAANVLEPREHALLLLLVYGPREGGRGAPDPFLGVKA AAAAELEERRYPG
TRLAWLAVRAEAPSQVRLMDVSVSKHPVDTLFFLTTVWTRPGPEVLRNRCRMNAISGWQAFFP
VHFQEFNPALSPQRSPPGPPGAGPDPPSPGADPSRGAPIGGRFDRQASAEFCFYNAADVLA
RARLAGELAGQQEEEALEGLEVMDVFLRFSGHLHFRAVEPGLVQKFSLRDCSPRLSEELYHR
CRLSNLEGLGGRAGLAMALFEEQANST

Signal sequence:

amino acids 1-15

Transmembrane domain:

amino acids 489-507

N-glycosylation site.

amino acids 121-125, 342-346

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 319-323, 464-468

Casein kinase II phosphorylation site.

amino acids 64-68, 150-154, 322-326, 331-337, 368-372, 385-389,
399-403, 409-413, 473-477, 729-733, 748-752

Tyrosine kinase phosphorylation site.

amino acids 736-743

N-myristoylation site.

amino acids 19-25, 23-29, 136-142, 397-403, 441-447, 544-550,
558-564, 651-657, 657-663, 672-678

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 14-25

Cell attachment sequence.

amino acids 247-250

090026515-071001

FIGURE 119

CGGAGTGGTGCACCGTGAAGGAAACCGTGCACGGCTGCCTTCTGTCCCCAAGCC
CTTCTAGACGCCGGAAAAATGCTTCTGAAAGCAGCTCTTTGAAGGGTGTGATGCTTGG
AACGATTTCTGTGCTTGATCACTATGCTAGGACACATTAGGATTGGTCAATGAAATAGAA
TGCACCAACCATGAGCATCATCACCTAACAGCTCTAACAAAGAAGATATCTGAAAATTCA
GAGGATGAGCGCATGGAGCTAGTAAGAGCTTCGAGTAACTGTATTATCCTGTAAACC
CAAAGATGTGAGTCTTGGGCTGCAGTAAGGAGACTTGGACCAACACTGTGACAAGCAG
AGTTCTCAGTCTGAAAATGTTAAAGTGTGAGTCATTAAATATGGACACAATGACATG
TGGTTAATGATGAGAAAAGCTTACAAATACGCCCTTGATAAGTATAGAGACCAATACA
GTTCTCCTTGACGCCCACTACGTTGCTATCATTGAAAACCTAAAGTATTTTGTAA
AAAAGGATCCATCACAGCCTTCTATCTAGGCCACACTATAAAATCTGGAGACCTTGAATAT
CTGGGTATGGAAGGAGAATTGCTTAAGTGTAGAATCAATGAAAAGACTTAACAGCCTTCT
CAATATCCAGAAAATGTCCTGAAACAGGGAGGGTGAATTGGAGATATCTGAAGATAAAC
AGCTAGCAGTTGCTGAAATATGCTGGAGTATTGCAAGAAAATGCAAGAGATGCTGATGGA
AAAGATGTATTTAATACCAAATCTGTTGGCTTCTATTAAAGAGGCAATGACTTATCACCC
CAACCAAGGTAGTAGAAGGCTGTTGTCAGATATGGCTTTACTTTAATGGACTGACTCCAA
ATCAGATGCACTGTGATGATGTTGGGTATACCGCCTTAGGGCATTTGGCATTTCAT
GATGCACTGGTTTCTTACCTCAAATGGTCTGACAATGACT**TGAGAAGTGGTAGAAAAGCG**
TGAATATGATCTTGTATAGGACGTGTTGTCATTATTGTAGTAGTAACATATCCAA
TACAGCTGTATGTTCTTTCTTCTAAATTTGGTGGCTTTCTTAAACACATGAACATTGAAATG
TCAGTAGTACATTTTAAATGAGGGTGGTTTTCTTAAACACATGAACATTGAAATG
TGGTGGAAAAGTGTAAAGATAATAATTGCAAAATAACTATTAAATAATTATAT
GTGATAAAATTCTAAATTATGAAACATTAGAAATCTGGGCACATATTGCTGATTGGTT
AAAAAAATTAAACAGGTCTTAGCGTTCAAGATATGCAAAATGATATCTTAGTGTGAATT
TGTGATTAAAGTAAACATTAGCTGTGTTCCCTTACTTCAATAACTGATTATGTTCT
AAGCCTCCCCAAGTCCAATGGATTGCTTCTCAAAATGTCACAACAGCAACTAAAGAAA
ATTAAGTGAAGTGGAAAAT

09002615-071001

FIGURE 120

MLSESSSFLKGVMLGSIFCALITMLGHIRIGHGNRMHHHEHHHLQAPNKEDILKISEDERME
LSKSFRVYCIILVKPKDVSLWAAVKETWTKHCDKAEFFSSENVKVFESINMDTNMDWLMMRK
AYKYAFDKYRDQYNWFFLARPTTFAIIENLKYFLLKKDPSQPFYLGHТИKSGDLEYVGMEGG
IVLSV ресурсы
KSVGLSIKEAMTYHPNQVVEGCCSDMAVTFNGLTPNQMHVMMYGVYRLRAFGHIFNDALVFL
PPNGSDND

Signal sequence:

amino acids 1-33

N-glycosylation site.

amino acids 121-125, 342-346

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 319-323, 464-468

Casein kinase II phosphorylation site.

amino acids 64-132, 150-154, 322-326, 331-335, 368-372, 385-389,
399-403, 409-413, 473-477, 729-733, 748-752

Tyrosine kinase phosphorylation site.

amino acids 736-743

N-myristoylation site.

amino acids 19-25, 23-29, 136-142, 397-403, 441-447, 544-550,
558-564, 651-657, 657-663, 672-672

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 14-25

Cell attachment sequence.

amino acids 247-250

FIGURE 121

CCACACGCGTCCGATCTTACCAACAAACACTCCGTGAGGGAGAAAGAGAGGGAGGGAGAG
AAAAAGAGAGAGAGAGAAACAAAAACCAAAGAGAGAGAAAAATGAATTCATCTAAATCAT
CTGAAACACAAATGCAAGAGAGAGGATGCTCTCTTCCAAATGTTCTATGGACTGTTGCT
GGGATCCCCATCCTATTTCTAGTGCCTGTTCATCACCAGATGTGTTGACATTGCGAT
CTTCAAACCTGTGATGAGAAAAAGTTCACTGAGAATTTCACAGAGCTCTCTGCT
ACAATTATGGATCAGGTTCACTGAGAATTGTTGTCATTGAACTGGGAATTTCATCC
AGCTGCTACTCTTTCTACTGACACCATTTCTGGGGCTTAAGTTAAAGAACCTGCTCAGC
CATGGGGGCTCACCTGGTGGTTATCAACTCACAGGAGGAGCAGGAATTCTTCTACAAAGA
AACCTAAATGAGAGAGTTTTTATTGGACTGTCACTGGGGCTAGTGGCA
TGGGTGGACGGCACACCTTGACAAAGTCTGTGAGCTCTGGGATGTAGGGAGGCCAACAA
CATAGCTACCTGGAGGACTGTGCCACCATGAGAGACTCTCAAACCCAAGGCAAATTGGA
ATGATGTAACCTGTTCTCAATTATTTGGATTGTGAAATGGTAGGAATAATCTTTG
AACAAAGGAAATCTTTAAGAACAGAAGGCACAACCTCAAATGTGAAAGAAGGAAGAGCA
AGAACATGGCCACACCCACGGCCCCACCGAGAAATTGTGCGCTGAACCTCAAAGGACTTC
ATAAGTATTGTTACTCTGATACAAATAAAATAAGTAGTTAAATGTTAAAAAAAAAAAA
AA
AAAAA

FIGURE 122

MNSSKSSETQCTERGCFSSQMFLWTVAGIPILFLSACFITRCVVTFRIFQTCDEKKFQLPEN
FTELSCYNYGGSVKNCCPLNWEYFQSSCYFFSTDTISWALSLKNCSAMGAHLVVINSQEEQ
EFLSYKKPKMREFFIGLSDQVVEGQWQWVDTPLTKSLSFWDVGEPPNNIATLEDCATMRDSS
NPRQNWNNDVTCFLNYFRICEMVGINPLNKGKSL

Signal sequence:

amino acids 1-42

N-glycosylation site.

amino acids 2-6, 62-66, 107-111

Casein kinase II phosphorylation site.

amino acids 51-55, 120-124, 163-167, 175-179, 181-185

N-myristoylation site.

amino acids 15-21, 74-80, 155-161

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 27-38

09902515-0710001

FIGURE 123

FIGURE 124

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77624
><subunit 1 of 1, 310 aa, 1 stop
><MW: 35020, PI: 7.90, NX(S/T): 3
MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQTSD
PRIEWKKIQDQEQTYYVFFDNKIQGDLAGRAEILGKTSLKIVNVTRRDSALYRCEVVARNDRK
EIDEIVIELTVQVKPVTPVCRVPKAVPGKMATLHCQESEGHPRPHYSWYRNDVPLPTDSRA
NPRFRNSSFHLNSETGTLVFTAHKDDSGQYYCIAASNDAGSARCEEQEMEVYDLNIGGIIGG
VILVVLAVLALITLGIICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEGDFRHKSSFVI
```

Important features of the protein:

Signal peptide:

amino acids 1-30

Transmembrane domain:

amino acids 243-263

N-glycosylation sites.

amino acids 104-107, 192-195

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 107-110

Casein kinase II phosphorylation site.

amino acids 106-109, 296-299

Tyrosine kinase phosphorylation site.

amino acids 69-77

N-myristoylation sites.

amino acids 26-31, 215-220, 226-231, 243-248, 244-249, 262-267